Cellular Expression of β_2AR-βgalΔα Fusion Protein in C2 Clones
(measured by anti-β-gal ELISA)

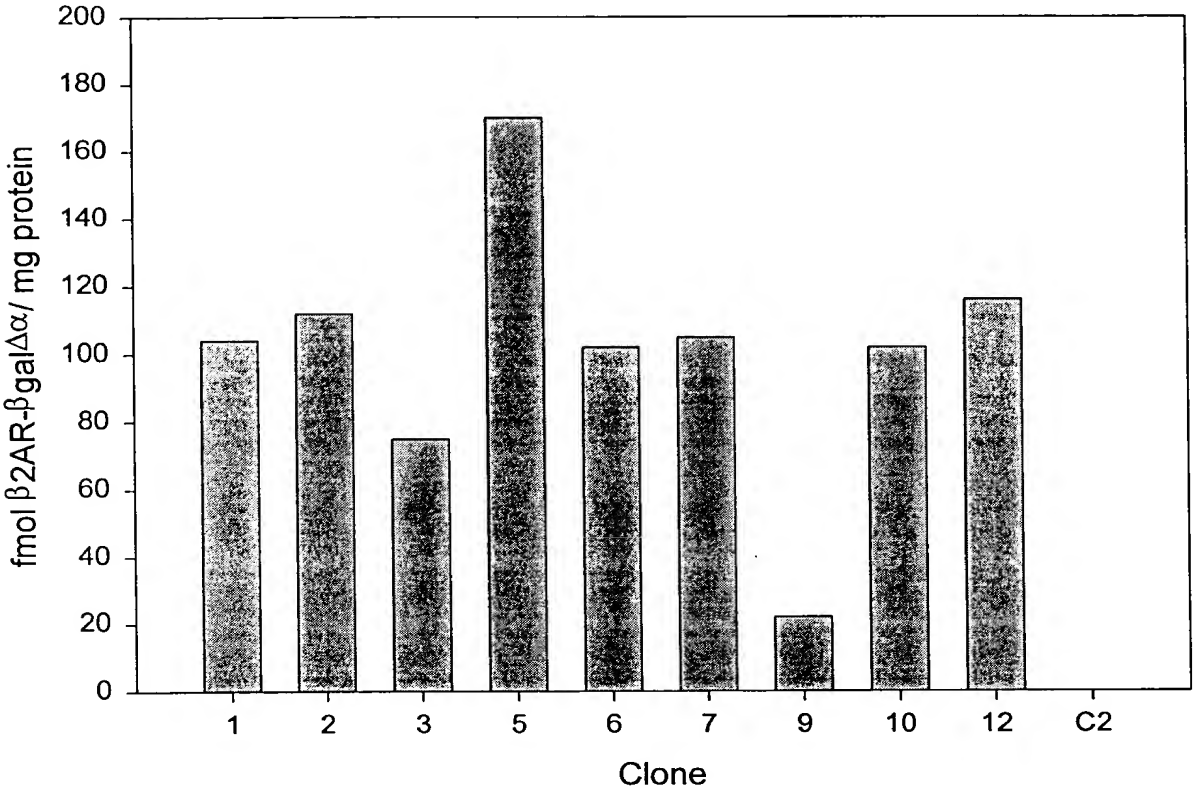

FIGURE 1A

Cellular expression of βArr2-βgalΔω fusion protein in C2 clones
(measured by anti-β gal ELISA)

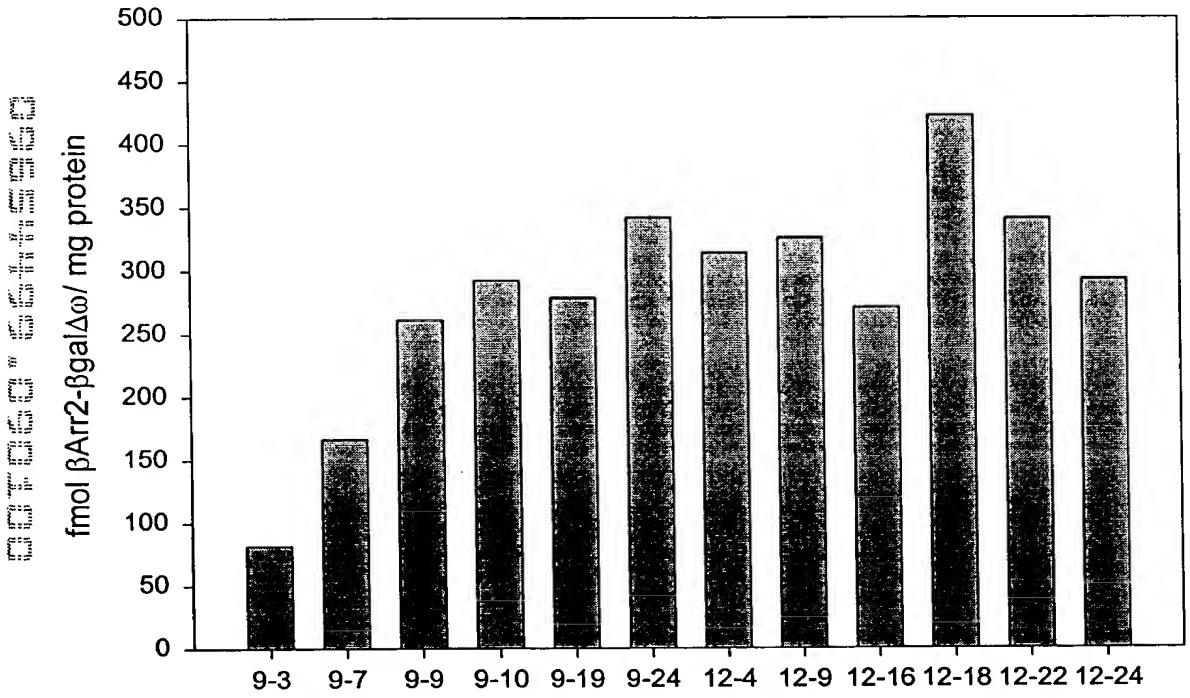

FIGURE 1B

Agonist Stimulated cAMP Response in C2 Cells Expressing β2AR-βgalΔα

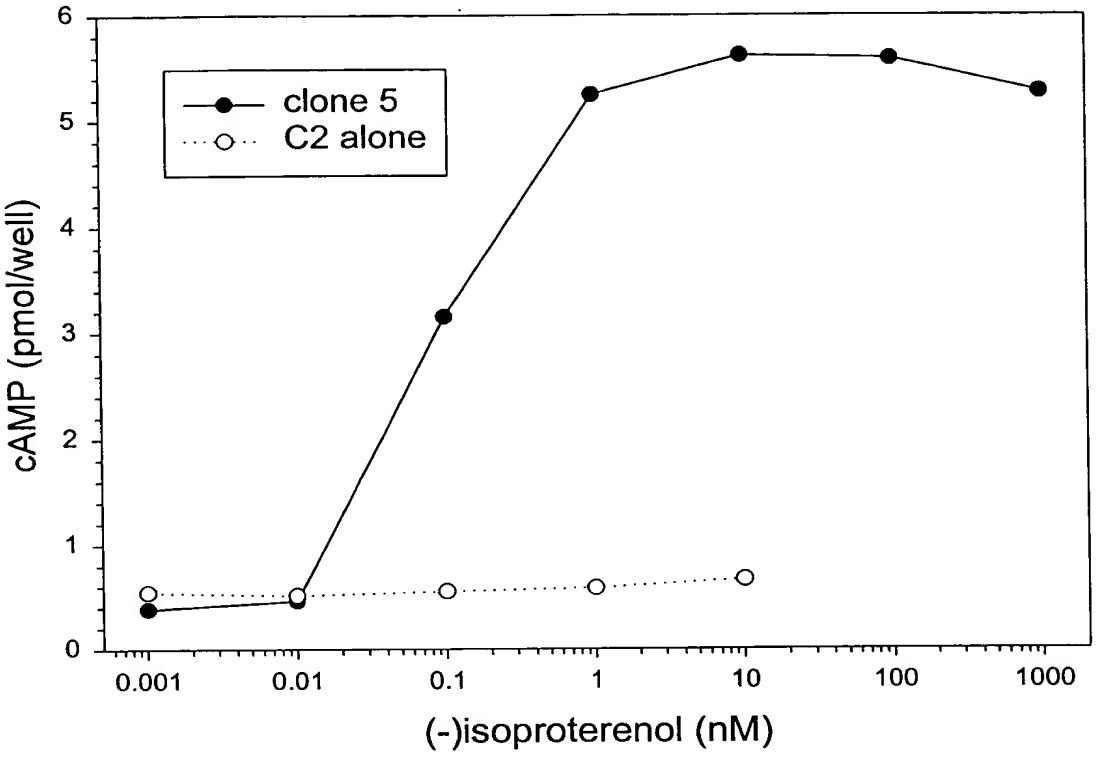

FIGURE 2

β–galactosidase Complementation as a Measurement for β2AR-βgalΔα interacting with βArrestin2-βgalΔω upon agonist Stimulation

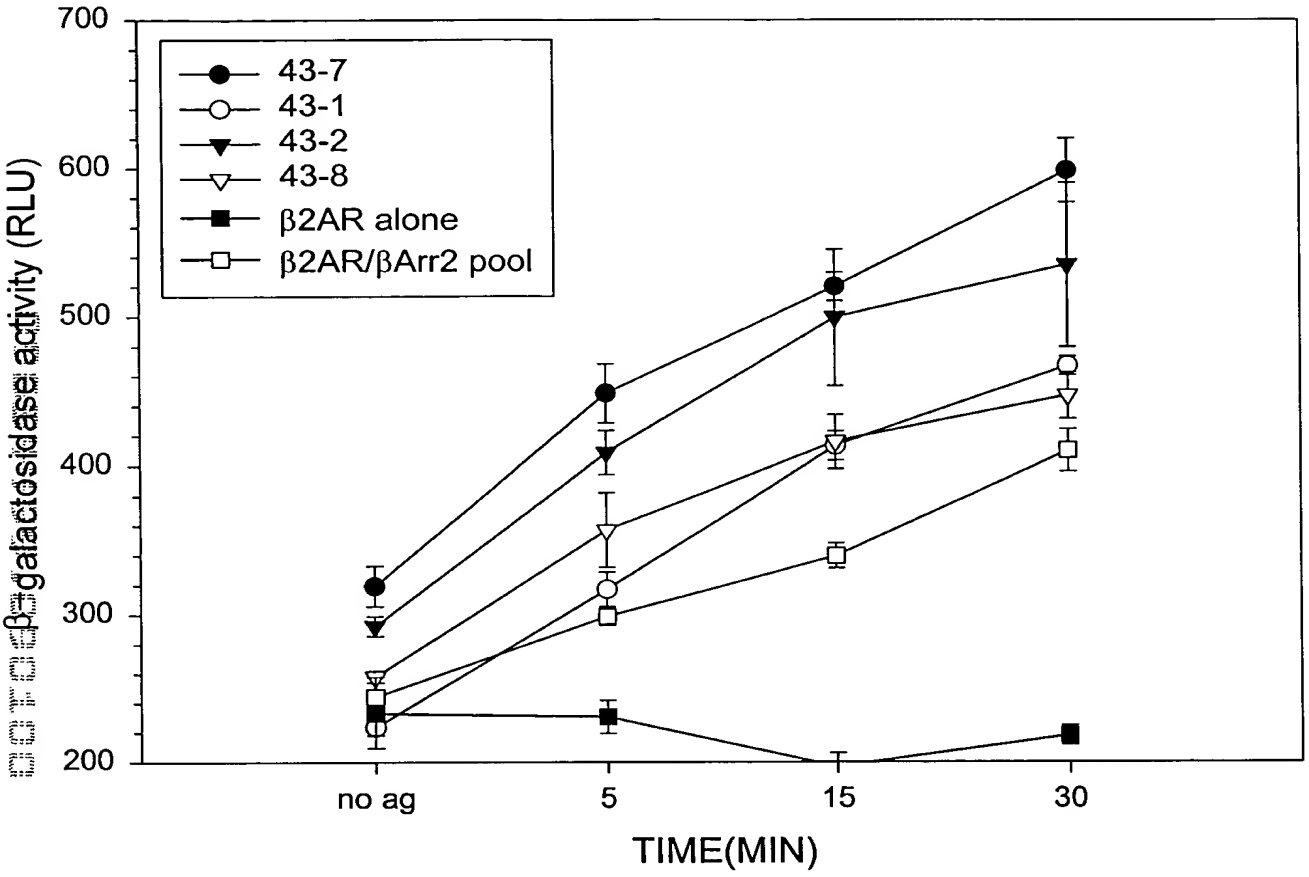

FIGURE 3A

β–galactosidase Complementation as a Measurement for β2AR-βgalΔα Interaction with βArrestin1-βgalΔω upon Agonist Stimulation

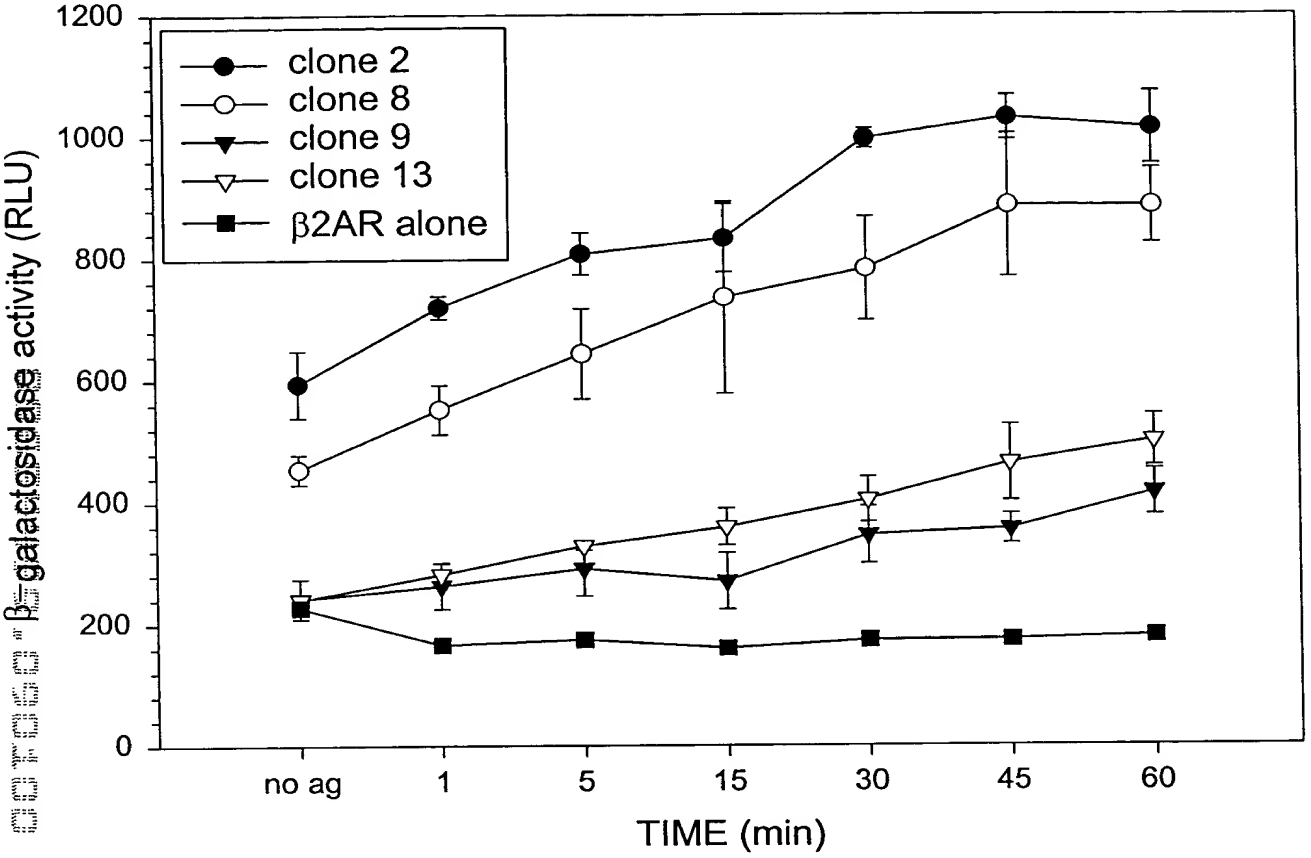

FIGURE 3B

β–galactosidase Activity in Response to Agonist in C2 Cells Coexpressing β2AR-βgalΔα and βArrestin2-βgalΔω Fusion Proteins

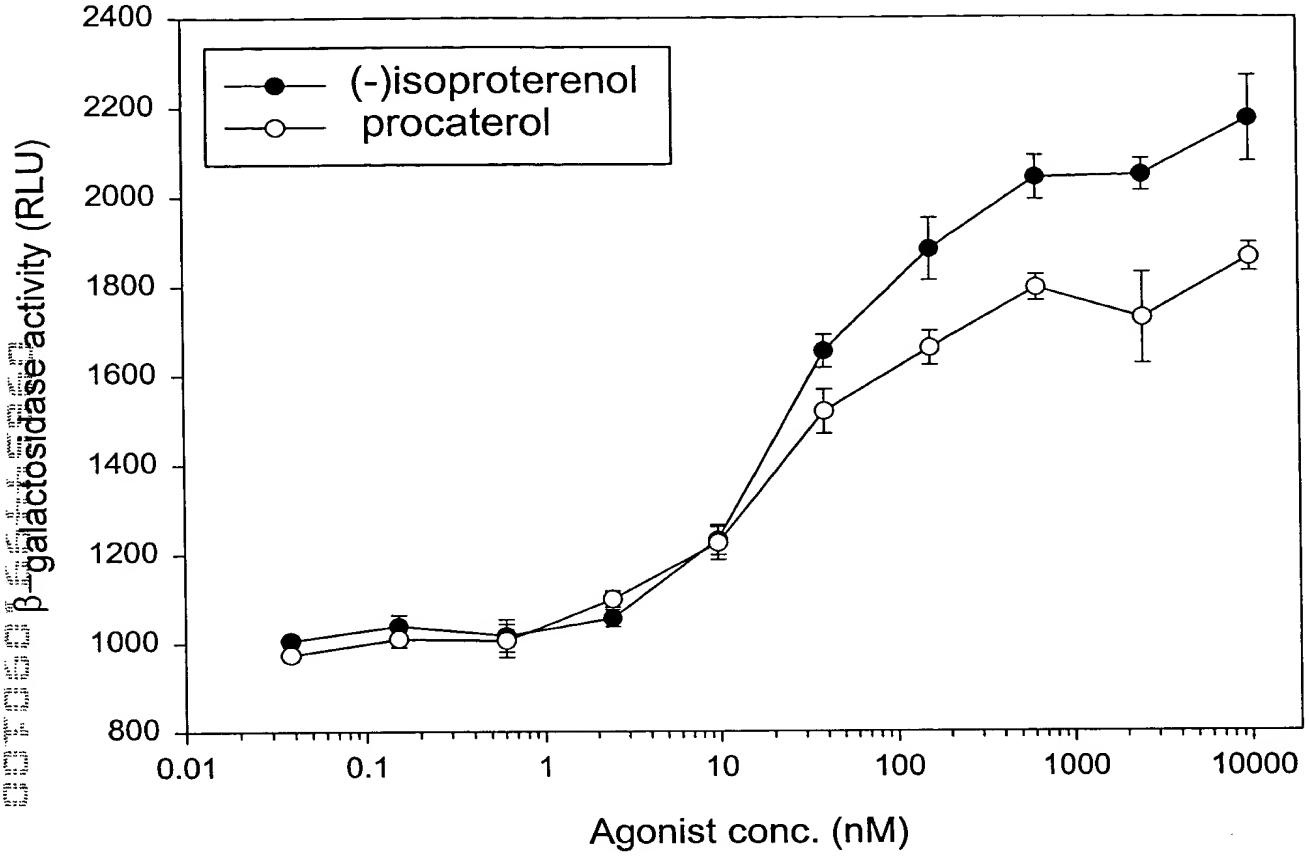

FIGURE 4A

β–galactosidase Activity in Response to Agonist in C2 Cells Coexpressing β2AR-βgalΔα and βArrestin1-βgalΔω Fusion Proteins

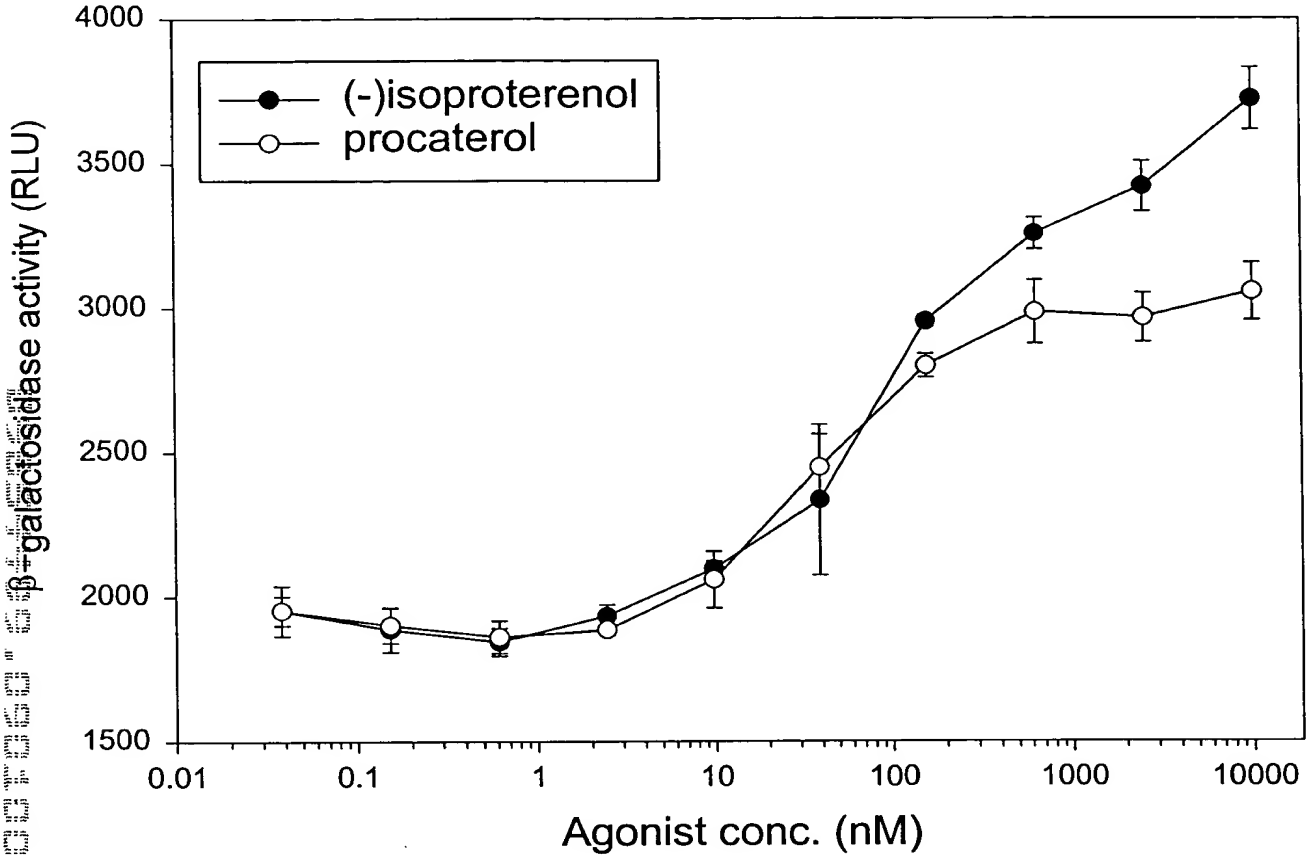

FIGURE 4B

Inhibition of β–galactosidase activity in C2 Cells Coexpressing β2AR–βgalΔα and βArrestin2-βgalΔω Fusion Proteins

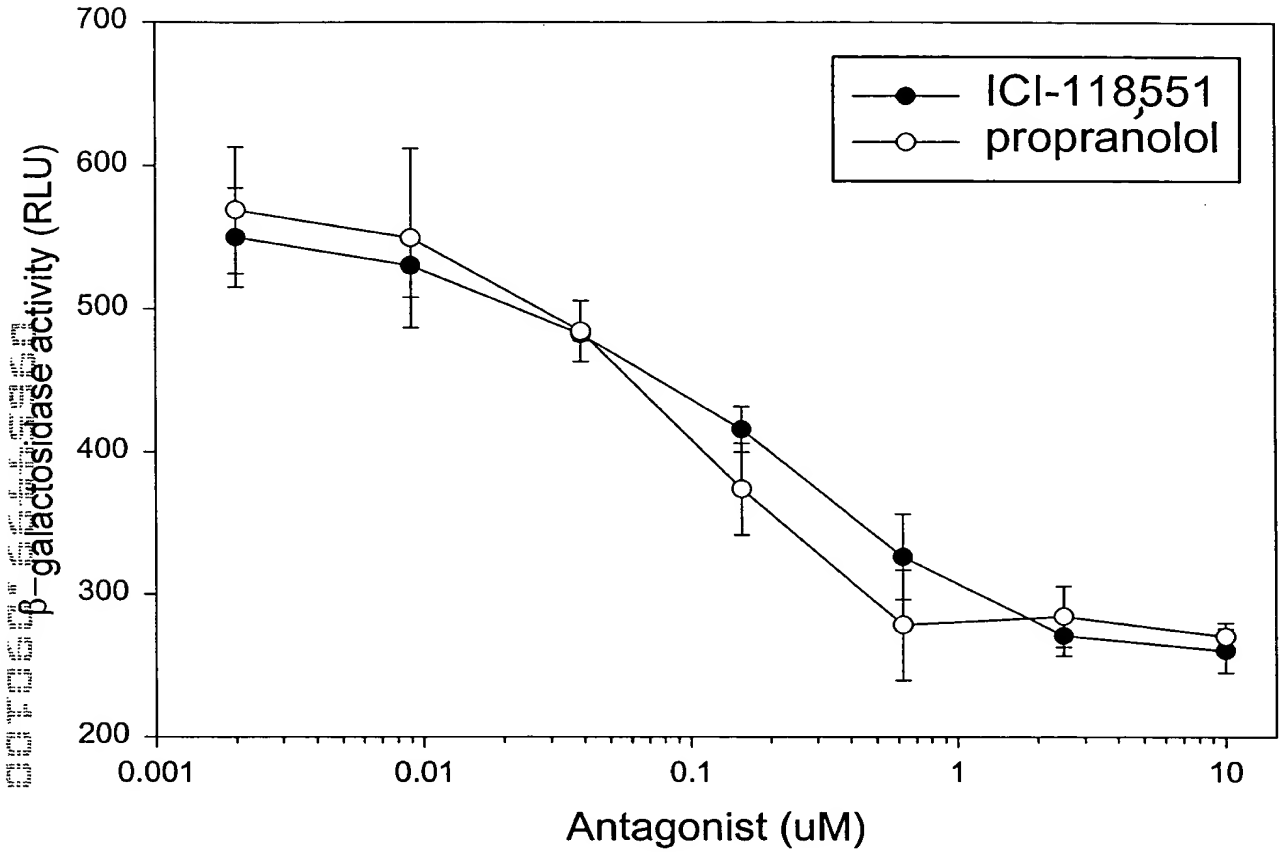

FIGURE 5A

Antagonist Inhibition of β–galactosidase Activity in C2 Cells Coexpressing β2AR-βgalΔα and βArrestin1-βgalΔω Fusion Proteins

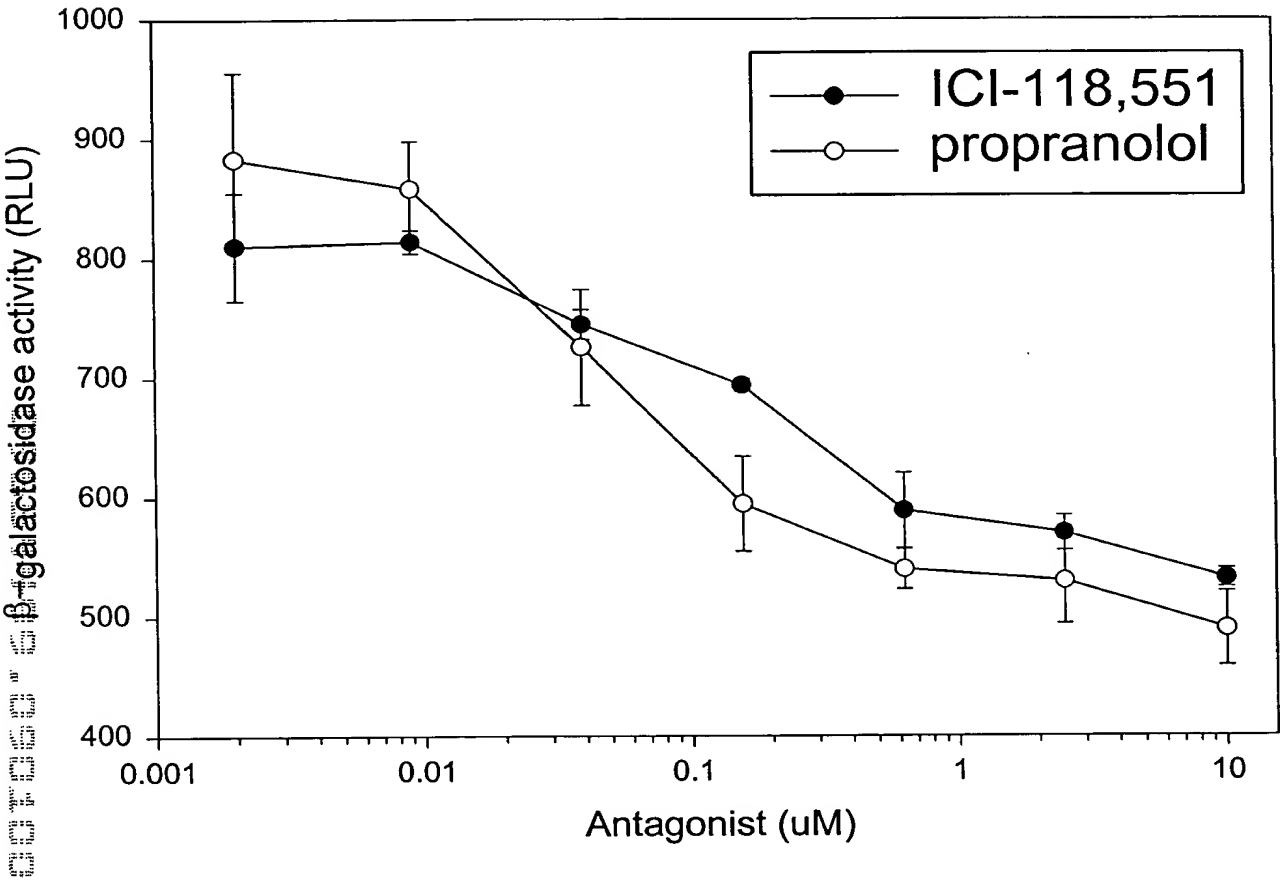

Figure 5B

Agonist Stimulated cAMP Response in Clones or Pools of C2 Cells Coexpressing A2aR-βgalΔα and βArrestin1-βgalΔω Fusion Proteins

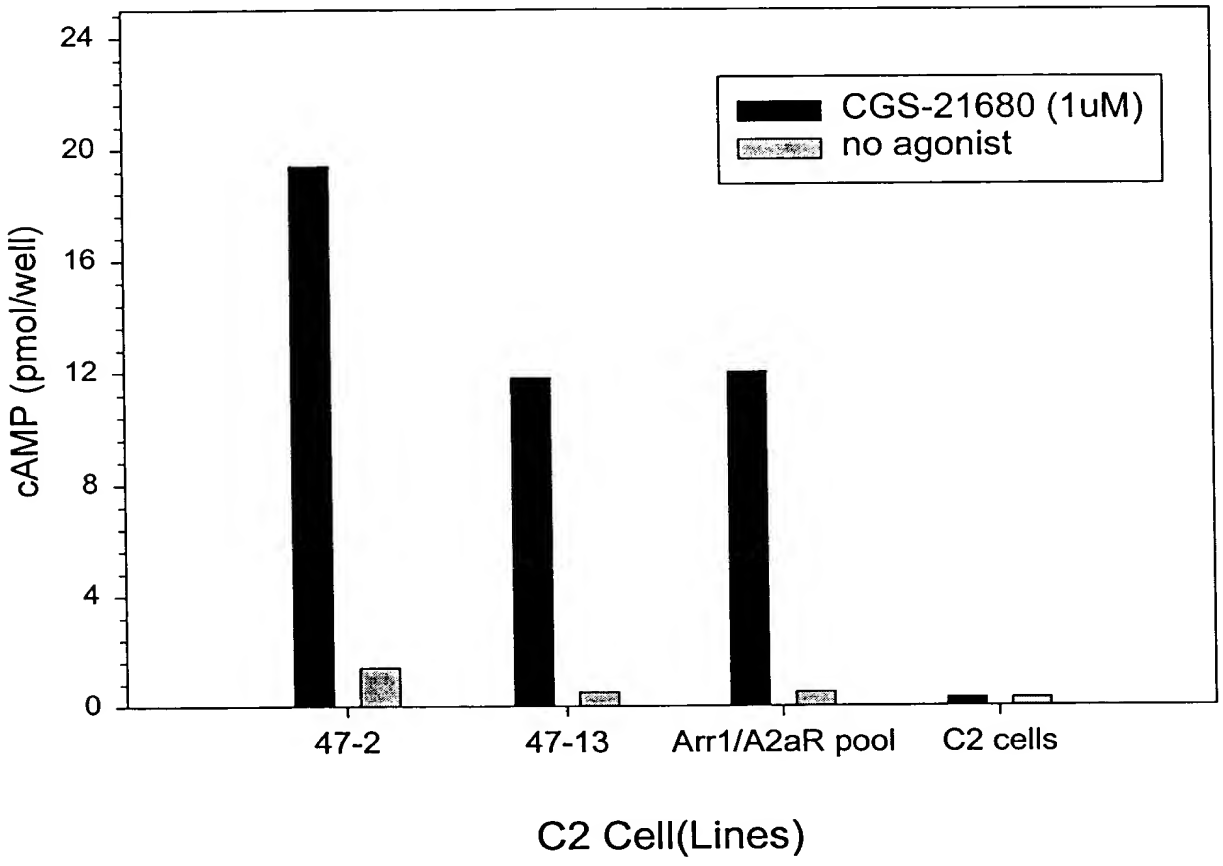

FIGURE 6

Agonist Stimulated cAMP Response in Clones or Pools of C2 Cells Expressing D1-βgalΔα and βArrestin2-βgalΔω Fusion Proteins

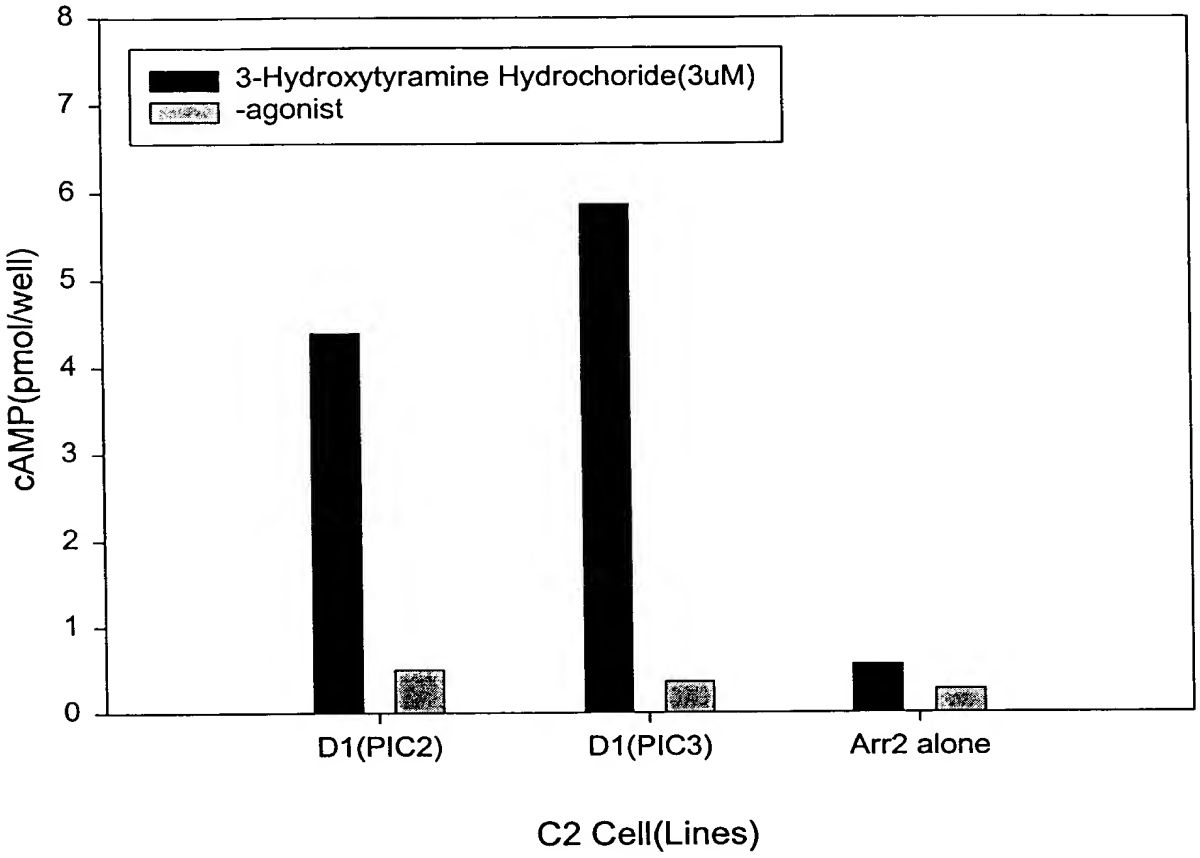

FIGURE 7

β_2AR-βgal$\Delta\omega$ and βarr2-βgal$\Delta\alpha$ Interaction in HEK293 Clones in Response to Isoproterenol Treatment (1 μM)

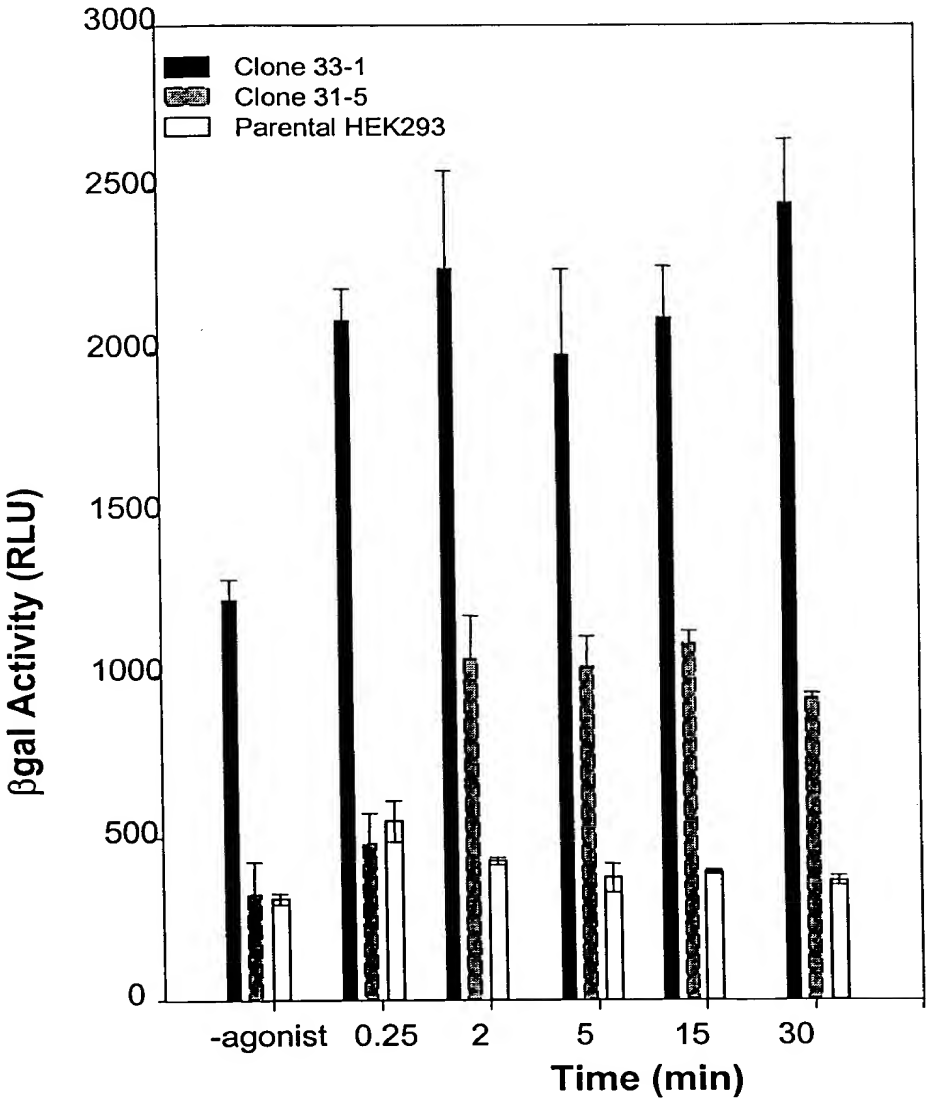

FIGURE 8A

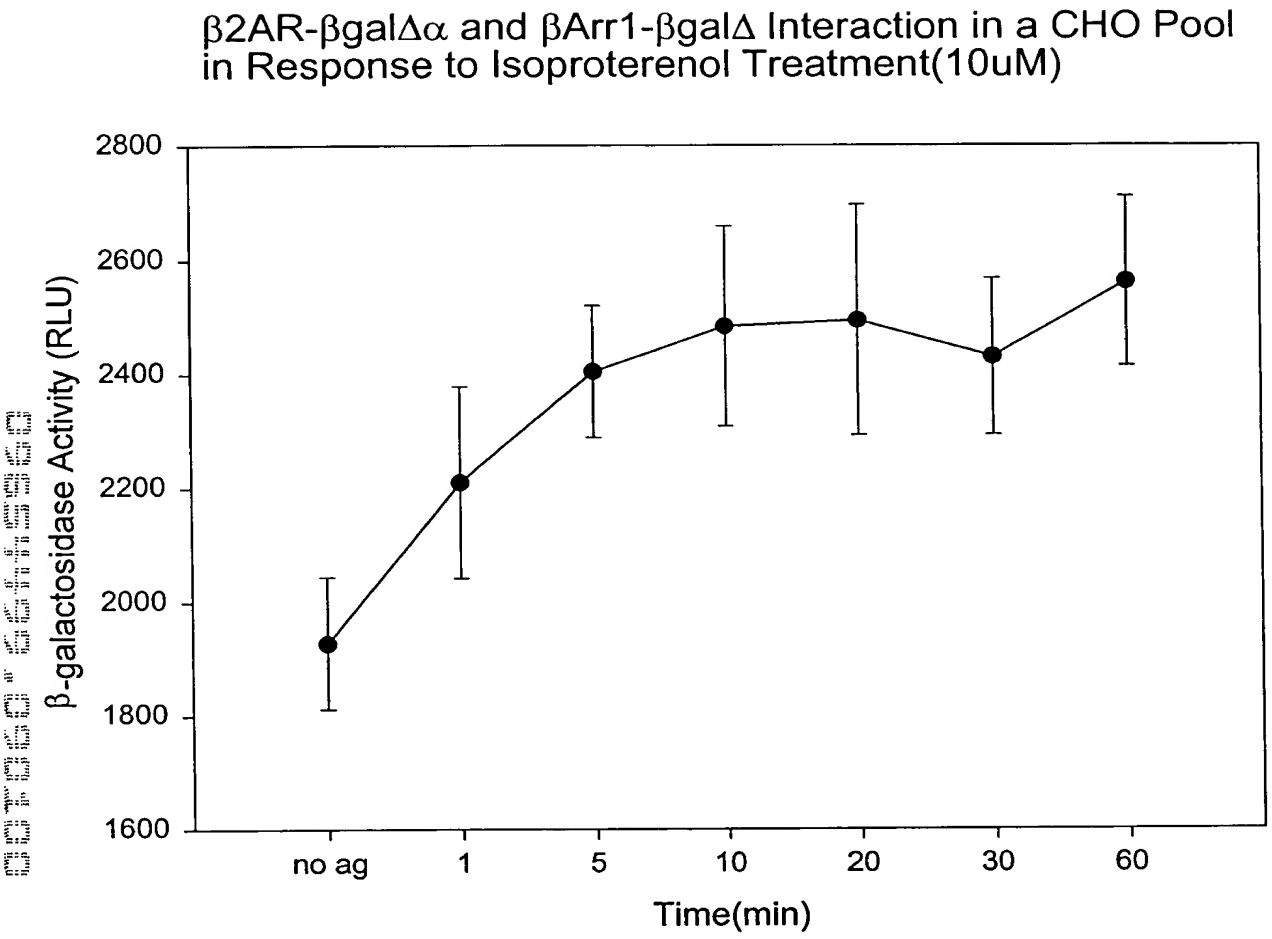
β2AR-βgalΔα and βArr1-βgalΔ Interaction in a CHO Pool in Response to Isoproterenol Treatment(10uM)
β-galactosidase Activity (RLU)
2800
2600
2400
2200
2000
1800
1600
no ag
1
5
10
20
30
60
Time(min)

FIGURE 8B

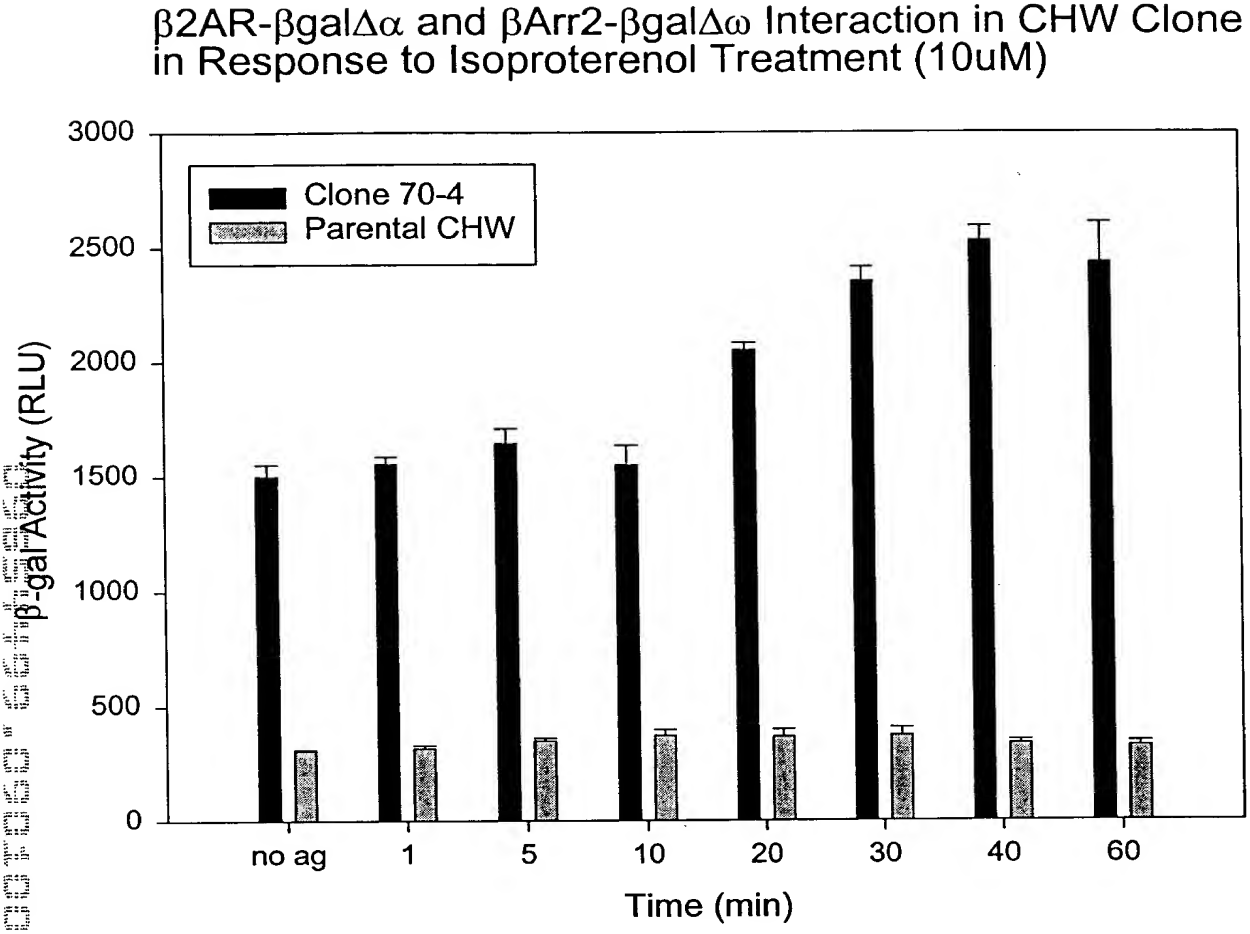
β2AR-βgalΔα and βArr2-βgalΔω Interaction in CHW Clone in Response to Isoproterenol Treatment (10uM)
Clone 70-4
Parental CHW
β-gal Activity (RLU)
3000
2500
2000
1500
1000
500
0
no ag
1
5
10
20
30
40
60
Time (min)

FIGURE 8C

β–galactosidase Complementation as a Measurement for Adrenergic Receptor Homodimerization in HEK 293 Cells Coexpressing β2AR-βgalΔα and β2AR-βgalΔω.

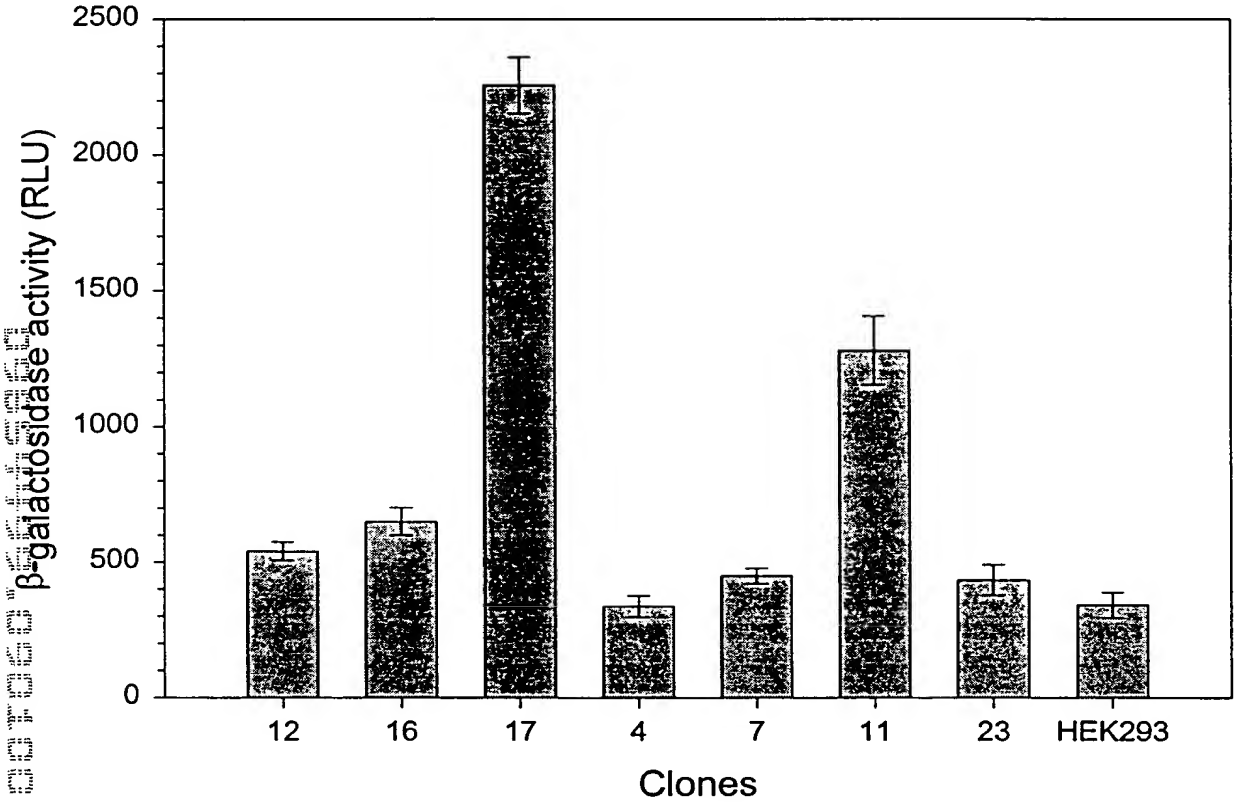

FIGURE 9A

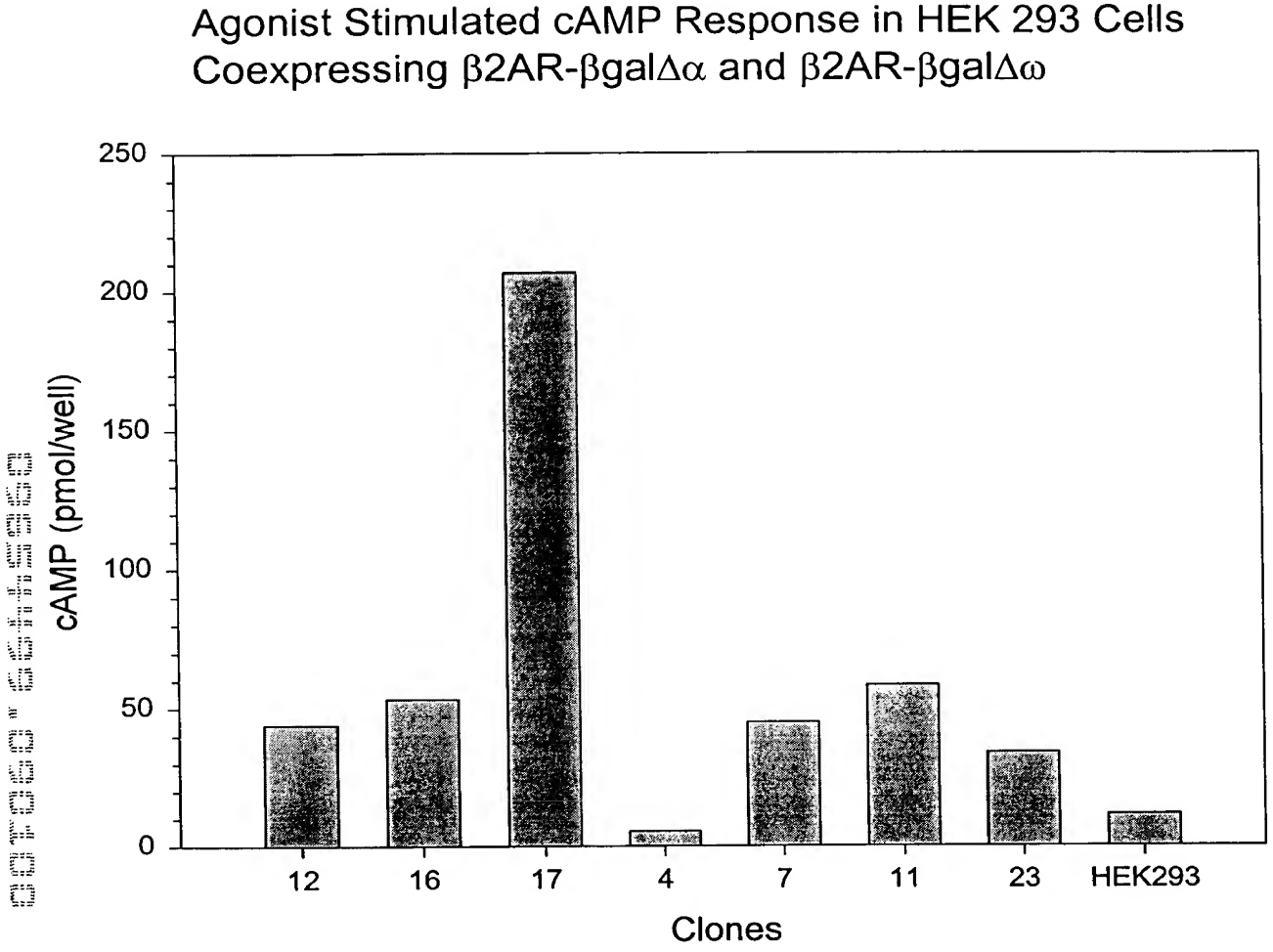
Agonist Stimulated cAMP Response in HEK 293 Cells
Coexpressing β2AR-βgalΔα and β2AR-βgalΔω
cAMP (pmol/well)
250
200
150
100
50
0
12
16
17
4
7
11
23
HEK293
Clones

FIGURE 9B

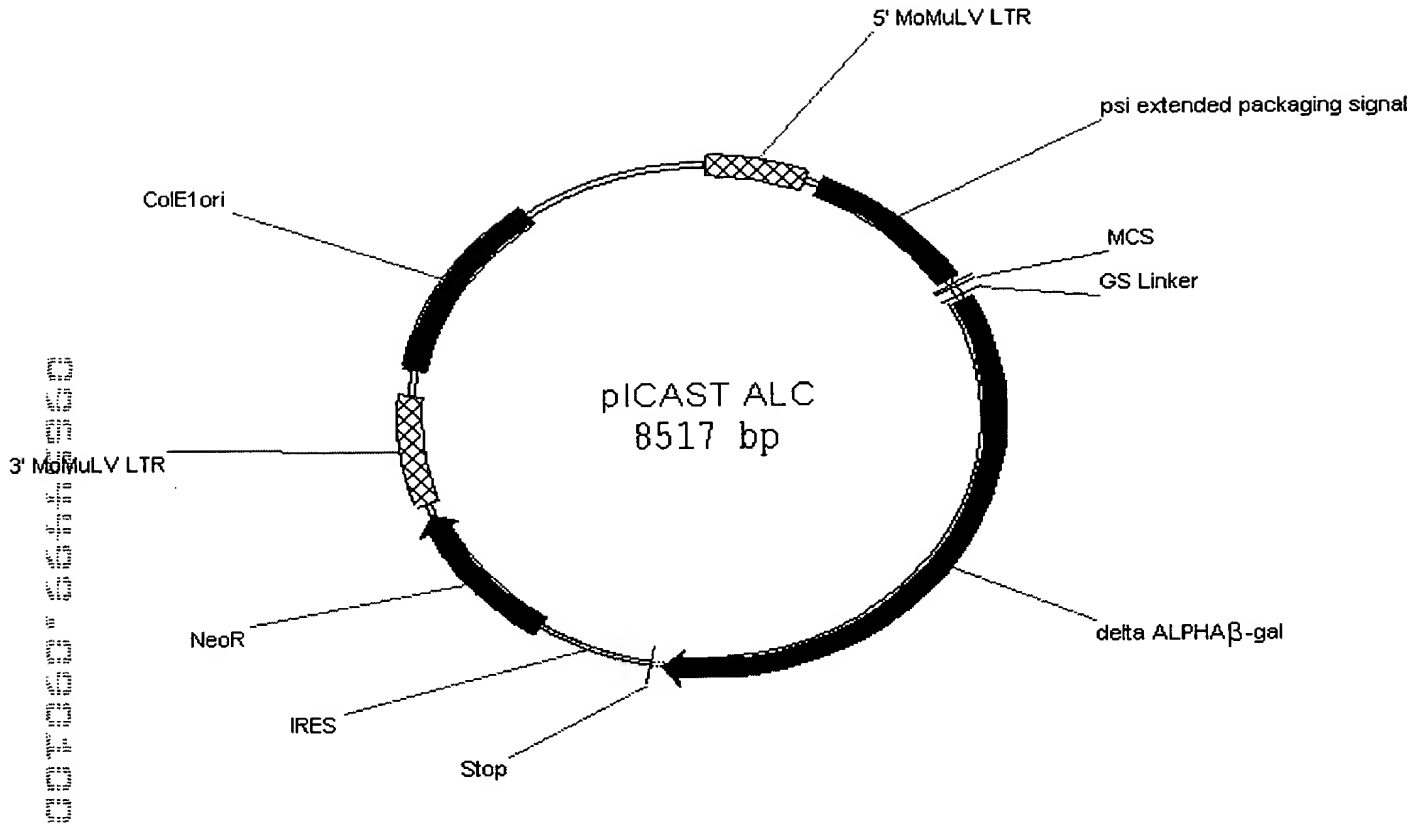
5' MoMuLV LTR
psi extended packaging signal
ColE1ori
MCS
GS Linker
pICAST ALC
8517 bp
3' MoMuLV LTR
NeoR
delta ALPHAβ-gal
IRES
Stop

Figure 10A

```
  1  CTGCAGCCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG
     GACGTCGGAC TTATACCCGG TTTGTCCTAT AGACACCATT CGTCAAGGAC
---------------------------------------------------------------------------
 51  CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA
     GGGGCCGAGT CCCGGTTCTT GTCTACCTTG TCGACTTATA CCCGGTTTGT
---------------------------------------------------------------------------
101  GGATATCTGT GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT
     CCTATAGACA CCATTCGTCA AGGACGGGGC CGAGTCCCGG TTCTTGTCTA
---------------------------------------------------------------------------
151  GGTCCCCAGA TGCGGTCCAG CCCTCAGCAG TTTCTAGAGA ACCATCAGAT
     CCAGGGGTCT ACGCCAGGTC GGGAGTCGTC AAAGATCTCT TGGTAGTCTA
---------------------------------------------------------------------------
201  GTTTCCAGGG TGCCCCAAGG ACCTGAAATG ACCCTGTGCC TTATTTGAAC
     CAAAGGTCCC ACGGGGTTCC TGGACTTTAC TGGGACACGG AATAAACTTG
---------------------------------------------------------------------------
251  TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC TGCTCCCCGA
     ATTGGTTAGT CAAGCGAAGA GCGAAGACAA GCGCGCGAAG ACGAGGGGCT
---------------------------------------------------------------------------
301  GCTCAATAAA AGAGCCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT
     CGAGTTATTT TCTCGGGTGT TGGGGAGTGA GCCCCGCGGT CAGGAGGCTA
---------------------------------------------------------------------------
351  TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCCT CTTGCAGTTG
     ACTGACTCAG CGGGCCCATG GGCACATAGG TTATTTGGGA GAACGTCAAC
---------------------------------------------------------------------------
401  CATCCGACTT GTGGTCTCGC TGTTCCTTGG GAGGGTCTCC TCTGAGTGAT
     GTAGGCTGAA CACCAGAGCG ACAAGGAACC CTCCCAGAGG AGACTCACTA
---------------------------------------------------------------------------
451  TGACTACCCG TCAGCGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATCGG
     ACTGATGGGC AGTCGCCCCC AGAAAGTAAA CCCCCGAGCA GGCCCTAGCC
---------------------------------------------------------------------------
501  GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG CAAGCTGGCC
     CTCTGGGGAC GGGTCCCTGG TGGCTGGGTG GTGGCCCTCC GTTCGACCGG
---------------------------------------------------------------------------
551  AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG ACTGATTTTA
     TCGTTGAATA GACACAGACA GGCTAACAGA TCACAGATAC TGACTAAAAT
---------------------------------------------------------------------------
601  TGCGCCTGCG TCGGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC
     ACGCGGACGC AGCCATGATC AATCGATTGA TCGAGACATA GACCGCCTGG
---------------------------------------------------------------------------
651  CGTGGTGGAA CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG
     GCACCACCTT GACTGCTCAA GACTTGTGGG CCGGCGTTGG GACCCTCTGC
---------------------------------------------------------------------------
701  TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG CCCGACCTGA GGAAGGGAGT
     AGGGTCCCTG AAACCCCCGG CAAAAACACC GGGCTGGACT CCTTCCCTCA
---------------------------------------------------------------------------
751  CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
     GCTACACCTT AGGCTGGGGC AGTCCTATAC ACCAAGACCA TCCTCTGCTC
---------------------------------------------------------------------------
801  AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA
     TTGGATTTTG TCAAGGGCGG AGGCAGACTT AAAAACGAAA GCCAAACCTT
---------------------------------------------------------------------------
851  CCGAAGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT
     GGCTTCGGCG CGCAGAACAG ACGACGTCGT AGCAAGACAC AACAGAGACA
---------------------------------------------------------------------------
901  CTGACTGTGT TTCTGTATTT GTCTGAAAAT TAGGGCCAGA CTGTTACCAC
     GACTGACACA AAGACATAAA CAGACTTTTA ATCCCGGTCT GACAATGGTG
---------------------------------------------------------------------------
```

FIGURE 10B

```
 951  TCCCTTAAGT TTGACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG
-------------------------------------------------------------------------------
1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
-------------------------------------------------------------------------------
1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
-------------------------------------------------------------------------------
1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
-------------------------------------------------------------------------------
1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
-------------------------------------------------------------------------------
1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
-------------------------------------------------------------------------------
1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
-------------------------------------------------------------------------------
1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
-------------------------------------------------------------------------------
1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAATCAGG
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTAGTCC
-------------------------------------------------------------------------------
1401  CCTTGGCGCG CCGGATCCTT AATTAAGCGC AATTGGGAGG TGGCGGTAGC
      GGAACCGCGC GGCCTAGGAA TTAATTCGCG TTAACCCTCC ACCGCCATCG
-------------------------------------------------------------------------------
 +2         M  G   V  I  T   D  S  L   A  V  V  A   R  T  D
           ]-------------------------------------------------
1451  CTCGAGATGG GCGTGATTAC GGATTCACTG GCCGTCGTGG CCCGCACCGA
      GAGCTCTACC CGCACTAATG CCTAAGTGAC CGGCAGCACC GGGCGTGGCT
-------------------------------------------------------------------------------
 +2   R  P  S   Q  Q  L  R   S  L  N   G  E  W   R  F  A
      ---------------------------------------------------
1501  TCGCCCTTCC CAACAGTTAC GCAGCCTGAA TGGCGAATGG CGCTTTGCCT
      AGCGGGAAGG GTTGTCAATG CGTCGGACTT ACCGCTTACC GCGAAACGGA
-------------------------------------------------------------------------------
 +2 W  F  P  A   P  E  A   V  P  E  S   W  L  E   C  D  L
    ---------------------------------------------------
1551  GGTTTCCGGC ACCAGAAGCG GTGCCGGAAA GCTGGCTGGA GTGCGATCTT
      CCAAAGGCCG TGGTCTTCGC CACGGCCTTT CGACCGACCT CACGCTAGAA
-------------------------------------------------------------------------------
 +2  P  E  A  D   T  V  V   V  P  S   N  W  Q  M   H  G  Y
     ---------------------------------------------------
1601  CCTGAGGCCG ATACTGTCGT CGTCCCCTCA AACTGGCAGA TGCACGGTTA
      GGACTCCGGC TATGACAGCA GCAGGGGAGT TTGACCGTCT ACGTGCCAAT
-------------------------------------------------------------------------------
 +2   D  A  P   I  Y  T  N   V  T  Y   P  I  T   V  N  P
      ---------------------------------------------------
1651  CGATGCGCCC ATCTACACCA ACGTGACCTA TCCCATTACG GTCAATCCGC
      GCTACGCGGG TAGATGTGGT TGCACTGGAT AGGGTAATGC CAGTTAGGCG
-------------------------------------------------------------------------------
```

```
   +2 P  F  V  P   T  E  N   P  T  G  C   Y  S  L   T  F  N
      ---------------------------------------------------
1701  CGTTTGTTCC CACGGAGAAT CCGACGGGTT GTTACTCGCT CACATTTAAT
      GCAAACAAGG GTGCCTCTTA GGCTGCCCAA CAATGAGCGA GTGTAAATTA
-------------------------------------------------------------------------------

   +2 V  D  E  S   W  L  Q   E  G  Q   T  R  I  I   F  D  G
      ---------------------------------------------------
1751  GTTGATGAAA GCTGGCTACA GGAAGGCCAG ACGCGAATTA TTTTTGATGG
      CAACTACTTT CGACCGATGT CCTTCCGGTC TGCGCTTAAT AAAAACTACC
-------------------------------------------------------------------------------

   +2   V  N  S   A  F  H  L   W  C  N   G  R  W   V  G  Y
      ---------------------------------------------------
1801  CGTTAACTCG GCGTTTCATC TGTGGTGCAA CGGGCGCTGG GTCGGTTACG
      GCAATTGAGC CGCAAAGTAG ACACCACGTT GCCCGCGACC CAGCCAATGC
-------------------------------------------------------------------------------

   +2 G  Q  D  S   R  L  P   S  E  F  D   L  S  A   F  L  R
      ---------------------------------------------------
1851  GCCAGGACAG TCGTTTGCCG TCTGAATTTG ACCTGAGCGC ATTTTTACGC
      CGGTCCTGTC AGCAAACGGC AGACTTAAAC TGGACTCGCG TAAAAATGCG
-------------------------------------------------------------------------------

   +2  A  G  E  N   R  L  A   V  M  V   L  R  W  S   D  G  S
      ---------------------------------------------------
1901  GCCGGAGAAA ACCGCCTCGC GGTGATGGTG CTGCGCTGGA GTGACGGCAG
      CGGCCTCTTT TGGCGGAGCG CCACTACCAC GACGCGACCT CACTGCCGTC
-------------------------------------------------------------------------------

   +2   Y  L  E   D  Q  D  M   W  R  M   S  G  I   F  R  D
      ---------------------------------------------------
1951  TTATCTGGAA GATCAGGATA TGTGGCGGAT GAGCGGCATT TTCCGTGACG
      AATAGACCTT CTAGTCCTAT ACACCGCCTA CTCGCCGTAA AAGGCACTGC
-------------------------------------------------------------------------------

   +2 V  S  L  L   H  K  P   T  T  Q   I  S  D  F   H  V  A
      ---------------------------------------------------
2001  TCTCGTTGCT GCATAAACCG ACTACACAAA TCAGCGATTT CCATGTTGCC
      AGAGCAACGA CGTATTTGGC TGATGTGTTT AGTCGCTAAA GGTACAACGG
-------------------------------------------------------------------------------

   +2  T  R  F  N   D  D  F   S  R  A   V  L  E  A   E  V  Q
      ---------------------------------------------------
2051  ACTCGCTTTA ATGATGATTT CAGCCGCGCT GTACTGGAGG CTGAAGTTCA
      TGAGCGAAAT TACTACTAAA GTCGGCGCGA CATGACCTCC GACTTCAAGT
-------------------------------------------------------------------------------

   +2   M  C  G   E  L  R  D   Y  L  R   V  T  V   S  L  W
      ---------------------------------------------------
2101  GATGTGCGGC GAGTTGCGTG ACTACCTACG GGTAACAGTT TCTTTATGGC
      CTACACGCCG CTCAACGCAC TGATGGATGC CCATTGTCAA AGAAATACCG
-------------------------------------------------------------------------------

   +2 Q  G  E  T   Q  V  A   S  G  T  A   P  F  G   G  E  I
      ---------------------------------------------------
2151  AGGGTGAAAC GCAGGTCGCC AGCGGCACCG CGCCTTTCGG CGGTGAAATT
      TCCCACTTTG CGTCCAGCGG TCGCCGTGGC GCGGAAAGCC GCCACTTTAA
-------------------------------------------------------------------------------

   +2  I  D  E  R   G  G  Y   A  D  R   V  T  L  R   L  N  V
      ---------------------------------------------------
2201  ATCGATGAGC GTGGTGGTTA TGCCGATCGC GTCACACTAC GTCTGAACGT
      TAGCTACTCG CACCACCAAT ACGGCTAGCG CAGTGTGATG CAGACTTGCA
-------------------------------------------------------------------------------

   +2   E  N  P   K  L  W  S   A  E  I   P  N  L   Y  R  A
      ---------------------------------------------------
2251  CGAAAACCCG AAACTGTGGA GCGCCGAAAT CCCGAATCTC TATCGTGCGG
      GCTTTTGGGC TTTGACACCT CGCGGCTTTA GGGCTTAGAG ATAGCACGCC
-------------------------------------------------------------------------------
```

```
   +2 V  V  E  L  H  T  A  D  G  T  L  I  E  A  E  A  C
      ---------------------------------------------------
2301  TGGTTGAACT GCACACCGCC GACGGCACGC TGATTGAAGC AGAAGCCTGC
      ACCAACTTGA CGTGTGGCGG CTGCCGTGCG ACTAACTTCG TCTTCGGACG
-------------------------------------------------------------------------------
   +2  D  V  G  F  R  E  V  R  I  E  N  G  L  L  L  L  N
      ---------------------------------------------------
2351  GATGTCGGTT TCCGCGAGGT GCGGATTGAA AATGGTCTGC TGCTGCTGAA
      CTACAGCCAA AGGCGCTCCA CGCCTAACTT TTACCAGACG ACGACGACTT
-------------------------------------------------------------------------------
   +2   G  K  P  L  L  I  R  G  V  N  R  H  E  H  H  P
      ---------------------------------------------------
2401  CGGCAAGCCG TTGCTGATTC GAGGCGTTAA CCGTCACGAG CATCATCCTC
      GCCGTTCGGC AACGACTAAG CTCCGCAATT GGCAGTGCTC GTAGTAGGAG
-------------------------------------------------------------------------------
   +2 L  H  G  Q  V  M  D  E  Q  T  M  V  Q  D  I  L  L
      ---------------------------------------------------
2451  TGCATGGTCA GGTCATGGAT GAGCAGACGA TGGTGCAGGA TATCCTGCTG
      ACGTACCAGT CCAGTACCTA CTCGTCTGCT ACCACGTCCT ATAGGACGAC
-------------------------------------------------------------------------------
   +2  M  K  Q  N  N  F  N  A  V  R  C  S  H  Y  P  N  H
      ---------------------------------------------------
2501  ATGAAGCAGA ACAACTTTAA CGCCGTGCGC TGTTCGCATT ATCCGAACCA
      TACTTCGTCT TGTTGAAATT GCGGCACGCG ACAAGCGTAA TAGGCTTGGT
-------------------------------------------------------------------------------
   +2   P  L  W  Y  T  L  C  D  R  Y  G  L  Y  V  V  D
      ---------------------------------------------------
2551  TCCGCTGTGG TACACGCTGT GCGACCGCTA CGGCCTGTAT GTGGTGGATG
      AGGCGACACC ATGTGCGACA CGCTGGCGAT GCCGGACATA CACCACCTAC
-------------------------------------------------------------------------------
   +2 E  A  N  I  E  T  H  G  M  V  P  M  N  R  L  T  D
      ---------------------------------------------------
2601  AAGCCAATAT TGAAACCCAC GGCATGGTGC CAATGAATCG TCTGACCGAT
      TTCGGTTATA ACTTTGGGTG CCGTACCACG GTTACTTAGC AGACTGGCTA
-------------------------------------------------------------------------------
   +2  D  P  R  W  L  P  A  M  S  E  R  V  T  R  M  V  Q
      ---------------------------------------------------
2651  GATCCGCGCT GGCTACCGGC GATGAGCGAA CGCGTAACGC GAATGGTGCA
      CTAGGCGCGA CCGATGGCCG CTACTCGCTT GCGCATTGCG CTTACCACGT
-------------------------------------------------------------------------------
   +2   R  D  R  N  H  P  S  V  I  I  W  S  L  G  N  E
      ---------------------------------------------------
2701  GCGCGATCGT AATCACCCGA GTGTGATCAT CTGGTCGCTG GGGAATGAAT
      CGCGCTAGCA TTAGTGGGCT CACACTAGTA GACCAGCGAC CCCTTACTTA
-------------------------------------------------------------------------------
   +2 S  G  H  G  A  N  H  D  A  L  Y  R  W  I  K  S  V
      ---------------------------------------------------
2751  CAGGCCACGG CGCTAATCAC GACGCGCTGT ATCGCTGGAT CAAATCTGTC
      GTCCGGTGCC GCGATTAGTG CTGCGCGACA TAGCGACCTA GTTTAGACAG
-------------------------------------------------------------------------------
   +2  D  P  S  R  P  V  Q  Y  E  G  G  G  A  D  T  T  A
      ---------------------------------------------------
2801  GATCCTTCCC GCCCGGTGCA GTATGAAGGC GGCGGAGCCG ACACCACGGC
      CTAGGAAGGG CGGGCCACGT CATACTTCCG CCGCCTCGGC TGTGGTGCCG
-------------------------------------------------------------------------------
   +2  T  D  I  I  C  P  M  Y  A  R  V  D  E  D  Q  P
      ---------------------------------------------------
2851  CACCGATATT ATTTGCCCGA TGTACGCGCG CGTGGATGAA GACCAGCCCT
      GTGGCTATAA TAAACGGGCT ACATGCGCGC GCACCTACTT CTGGTCGGGA
-------------------------------------------------------------------------------
```

```
   +2 F  P  A  V   P  K  W   S  I  K  K   W  L  S   L  P  G
      ---------------------------------------------------
2901  TCCCGGCTGT GCCGAAATGG TCCATCAAAA AATGGCTTTC GCTACCTGGA
      AGGGCCGACA CGGCTTTACC AGGTAGTTTT TTACCGAAAG CGATGGACCT
-------------------------------------------------------------------------------
   +2  E  T  R  P   L  I  L   C  E  Y   A  H  A  M   G  N  S
      ---------------------------------------------------
2951  GAGACGCGCC CGCTGATCCT TTGCGAATAC GCCCACGCGA TGGGTAACAG
      CTCTGCGCGG GCGACTAGGA AACGCTTATG CGGGTGCGCT ACCCATTGTC
-------------------------------------------------------------------------------
   +2   L  G  G   F  A  K  Y   W  Q  A   F  R  Q   Y  P  R
      ---------------------------------------------------
3001  TCTTGGCGGT TTCGCTAAAT ACTGGCAGGC GTTTCGTCAG TATCCCCGTT
      AGAACCGCCA AAGCGATTTA TGACCGTCCG CAAAGCAGTC ATAGGGGCAA
-------------------------------------------------------------------------------
   +2 L  Q  G  G   F  V  W   D  W  V  D   Q  S  L   I  K  Y
      ---------------------------------------------------
3051  TACAGGGCGG CTTCGTCTGG GACTGGGTGG ATCAGTCGCT GATTAAATAT
      ATGTCCCGCC GAAGCAGACC CTGACCCACC TAGTCAGCGA CTAATTTATA
-------------------------------------------------------------------------------
   +2  D  E  N  G   N  P  W   S  A  Y   G  G  D  F   G  D  T
      ---------------------------------------------------
3101  GATGAAAACG GCAACCCGTG GTCGGCTTAC GGCGGTGATT TTGGCGATAC
      CTACTTTTGC CGTTGGGCAC CAGCCGAATG CCGCCACTAA AACCGCTATG
-------------------------------------------------------------------------------
   +2   P  N  D   R  Q  F  C   M  N  G   L  V  F   A  D  R
      ---------------------------------------------------
3151  GCCGAACGAT CGCCAGTTCT GTATGAACGG TCTGGTCTTT GCCGACCGCA
      CGGCTTGCTA GCGGTCAAGA CATACTTGCC AGACCAGAAA CGGCTGGCGT
-------------------------------------------------------------------------------
   +2 T  P  H  P   A  L  T   E  A  K  H   Q  Q  Q   F  F  Q
      ---------------------------------------------------
3201  CGCCGCATCC AGCGCTGACG GAAGCAAAAC ACCAGCAGCA GTTTTTCCAG
      GCGGCGTAGG TCGCGACTGC CTTCGTTTTG TGGTCGTCGT CAAAAAGGTC
-------------------------------------------------------------------------------
   +2  F  R  L  S   G  Q  T   I  E  V   T  S  E  Y   L  F  R
      ---------------------------------------------------
3251  TTCCGTTTAT CCGGGCAAAC CATCGAAGTG ACCAGCGAAT ACCTGTTCCG
      AAGGCAAATA GGCCCGTTTG GTAGCTTCAC TGGTCGCTTA TGGACAAGGC
-------------------------------------------------------------------------------
   +2   H  S  D   N  E  L  L   H  W  M   V  A  L   D  G  K
      ---------------------------------------------------
3301  TCATAGCGAT AACGAGCTCC TGCACTGGAT GGTGGCGCTG GATGGTAAGC
      AGTATCGCTA TTGCTCGAGG ACGTGACCTA CCACCGCGAC CTACCATTCG
-------------------------------------------------------------------------------
   +2 P  L  A  S   G  E  V   P  L  D  V   A  P  Q   G  K  Q
      ---------------------------------------------------
3351  CGCTGGCAAG CGGTGAAGTG CCTCTGGATG TCGCTCCACA AGGTAAACAG
      GCGACCGTTC GCCACTTCAC GGAGACCTAC AGCGAGGTGT TCCATTTGTC
-------------------------------------------------------------------------------
   +2  L  I  E  L   P  E  L   P  Q  P   E  S  A  G   Q  L  W
      ---------------------------------------------------
3401  TTGATTGAAC TGCCTGAACT ACCGCAGCCG GAGAGCGCCG GGCAACTCTG
      AACTAACTTG ACGGACTTGA TGGCGTCGGC CTCTCGCGGC CCGTTGAGAC
-------------------------------------------------------------------------------
   +2  L  T  V   R  V  V  Q   P  N  A   T  A  W   S  E  A
      ---------------------------------------------------
3451  GCTCACAGTA CGCGTAGTGC AACCGAACGC GACCGCATGG TCAGAAGCCG
      CGAGTGTCAT GCGCATCACG TTGGCTTGCG CTGGCGTACC AGTCTTCGGC
-------------------------------------------------------------------------------
```

```
   +2 G  H  I  S  A  W  Q  Q  W  R  L  A  E  N  L  S  V
      ------------------------------------------------
3501  GGCACATCAG CGCCTGGCAG CAGTGGCGTC TGGCGGAAAA CCTCAGTGTG
      CCGTGTAGTC GCGGACCGTC GTCACCGCAG ACCGCCTTTT GGAGTCACAC
-------------------------------------------------------------------------------
   +2  T  L  P  A  A  S  H  A  I  P  H  L  T  T  S  E  M
      ------------------------------------------------
3551  ACGCTCCCCG CCGCGTCCCA CGCCATCCCG CATCTGACCA CCAGCGAAAT
      TGCGAGGGGC GGCGCAGGGT GCGGTAGGGC GTAGACTGGT GGTCGCTTTA
-------------------------------------------------------------------------------
   +2   D  F  C  I  E  L  G  N  K  R  W  Q  F  N  R  Q
      ------------------------------------------------
3601  GGATTTTTGC ATCGAGCTGG GTAATAAGCG TTGGCAATTT AACCGCCAGT
      CCTAAAAACG TAGCTCGACC CATTATTCGC AACCGTTAAA TTGGCGGTCA
-------------------------------------------------------------------------------
   +2 S  G  F  L  S  Q  M  W  I  G  D  K  K  Q  L  L  T
      ------------------------------------------------
3651  CAGGCTTTCT TTCACAGATG TGGATTGGCG ATAAAAAACA ACTGCTGACG
      GTCCGAAAGA AAGTGTCTAC ACCTAACCGC TATTTTTTGT TGACGACTGC
-------------------------------------------------------------------------------
   +2  P  L  R  D  Q  F  T  R  A  P  L  D  N  D  I  G  V
      ------------------------------------------------
3701  CCGCTGCGCG ATCAGTTCAC CCGTGCACCG CTGGATAACG ACATTGGCGT
      GGCGACGCGC TAGTCAAGTG GGCACGTGGC GACCTATTGC TGTAACCGCA
-------------------------------------------------------------------------------
   +2   S  E  A  T  R  I  D  P  N  A  W  V  E  R  W  K
      ------------------------------------------------
3751  AAGTGAAGCG ACCCGCATTG ACCCTAACGC CTGGGTCGAA CGCTGGAAGG
      TTCACTTCGC TGGGCGTAAC TGGGATTGCG GACCCAGCTT GCGACCTTCC
-------------------------------------------------------------------------------
   +2 A  A  G  H  Y  Q  A  E  A  A  L  L  Q  C  T  A  D
      ------------------------------------------------
3801  CGGCGGGCCA TTACCAGGCC GAAGCAGCGT TGTTGCAGTG CACGGCAGAT
      GCCGCCCGGT AATGGTCCGG CTTCGTCGCA ACAACGTCAC GTGCCGTCTA
-------------------------------------------------------------------------------
   +2  T  L  A  D  A  V  L  I  T  T  A  H  A  W  Q  H  Q
      ------------------------------------------------
3851  ACACTTGCTG ATGCGGTGCT GATTACGACC GCTCACGCGT GGCAGCATCA
      TGTGAACGAC TACGCCACGA CTAATGCTGG CGAGTGCGCA CCGTCGTAGT
-------------------------------------------------------------------------------
   +2   G  K  T  L  F  I  S  R  K  T  Y  R  I  D  G  S
      ------------------------------------------------
3901  GGGGAAAACC TTATTTATCA GCCGGAAAAC CTACCGGATT GATGGTAGTG
      CCCCTTTTGG AATAAATAGT CGGCCTTTTG GATGGCCTAA CTACCATCAC
-------------------------------------------------------------------------------
   +2 G  Q  M  A  I  T  V  D  V  E  V  A  S  D  T  P  H
      ------------------------------------------------
3951  GTCAAATGGC GATTACCGTT GATGTTGAAG TGGCGAGCGA TACACCGCAT
      CAGTTTACCG CTAATGGCAA CTACAACTTC ACCGCTCGCT ATGTGGCGTA
-------------------------------------------------------------------------------
   +2  P  A  R  I  G  L  N  C  Q  L  A  Q  V  A  E  R  V
      ------------------------------------------------
4001  CCGGCGCGGA TTGGCCTGAA CTGCCAGCTG GCGCAGGTAG CAGAGCGGGT
      GGCCGCGCCT AACCGGACTT GACGGTCGAC CGCGTCCATC GTCTCGCCCA
-------------------------------------------------------------------------------
   +2  N  W  L  G  L  G  P  Q  E  N  Y  P  D  R  L  T
      ------------------------------------------------
4051  AAACTGGCTC GGATTAGGGC CGCAAGAAAA CTATCCCGAC CGCCTTACTG
      TTTGACCGAG CCTAATCCCG GCGTTCTTTT GATAGGGCTG GCGGAATGAC
-------------------------------------------------------------------------------
```

```
   +2 A  A  C  F   D  R  W   D  L  P  L   S  D  M   Y  T  P
      ---------------------------------------------------
4101  CCGCCTGTTT TGACCGCTGG GATCTGCCAT TGTCAGACAT GTATACCCCG
      GGCGGACAAA ACTGGCGACC CTAGACGGTA ACAGTCTGTA CATATGGGGC
-------------------------------------------------------------------------------

   +2  Y  V  F  P   S  E  N   G  L  R   C  G  T  R   E  L  N
      ---------------------------------------------------
4151  TACGTCTTCC CGAGCGAAAA CGGTCTGCGC TGCGGGACGC GCGAATTGAA
      ATGCAGAAGG GCTCGCTTTT GCCAGACGCG ACGCCCTGCG CGCTTAACTT
-------------------------------------------------------------------------------

   +2    Y  G  P   H  Q  W  R   G  D  F   Q  F  N   I  S  R
      ---------------------------------------------------
4201  TTATGGCCCA CACCAGTGGC GCGGCGACTT CCAGTTCAAC ATCAGCCGCT
      AATACCGGGT GTGGTCACCG CGCCGCTGAA GGTCAAGTTG TAGTCGGCGA
-------------------------------------------------------------------------------

   +2 Y  S  Q  Q   Q  L  M   E  T  S  H   R  H  L   L  H  A
      ---------------------------------------------------
4251  ACAGTCAACA GCAACTGATG GAAACCAGCC ATCGCCATCT GCTGCACGCG
      TGTCAGTTGT CGTTGACTAC CTTTGGTCGG TAGCGGTAGA CGACGTGCGC
-------------------------------------------------------------------------------

   +2  E  E  G  T   W  L  N   I  D  G   F  H  M  G   I  G  G
      ---------------------------------------------------
4301  GAAGAAGGCA CATGGCTGAA TATCGACGGT TTCCATATGG GGATTGGTGG
      CTTCTTCCGT GTACCGACTT ATAGCTGCCA AAGGTATACC CCTAACCACC
-------------------------------------------------------------------------------

   +2   D  D  S   W  S  P  S   V  S  A   E  F  Q   L  S  A
      ---------------------------------------------------
4351  CGACGACTCC TGGAGCCCGT CAGTATCGGC GGAATTCCAG CTGAGCGCCG
      GCTGCTGAGG ACCTCGGGCA GTCATAGCCG CCTTAAGGTC GACTCGCGGC
-------------------------------------------------------------------------------

   +2 G  R  Y  H   Y  Q  L   V  W  C  Q   K  R  S   D  Y  K
      ---------------------------------------------------
4401  GTCGCTACCA TTACCAGTTG GTCTGGTGTC AAAAAAGATC TGACTATAAA
      CAGCGATGGT AATGGTCAAC CAGACCACAG TTTTTTCTAG ACTGATATTT
-------------------------------------------------------------------------------

   +2  D  E  D  L   D  H  H   H  H  H   H  R
      ------------------------------------>
4451  GATGAGGACC TCGACCATCA TCATCATCAT CACCGGTAAT AATAGGTAGA
      CTACTCCTGG AGCTGGTAGT AGTAGTAGTA GTGGCCATTA TTATCCATCT
-------------------------------------------------------------------------------

4501  TAAGTGACTG ATTAGATGCA TTGATCCCTC GACCAATTCC GGTTATTTTC
      ATTCACTGAC TAATCTACGT AACTAGGGAG CTGGTTAAGG CCAATAAAAG
-------------------------------------------------------------------------------

4551  CACCATATTG CCGTCTTTTG GCAATGTGAG GGCCCGGAAA CCTGGCCCTG
      GTGGTATAAC GGCAGAAAAC CGTTACACTC CCGGGCCTTT GGACCGGGAC
-------------------------------------------------------------------------------

4601  TCTTCTTGAC GAGCATTCCT AGGGGTCTTT CCCCTCTCGC CAAAGGAATG
      AGAAGAACTG CTCGTAAGGA TCCCCAGAAA GGGGAGAGCG GTTTCCTTAC
-------------------------------------------------------------------------------

4651  CAAGGTCTGT TGAATGTCGT GAAGGAAGCA GTTCCTCTGG AAGCTTCTTG
      GTTCCAGACA ACTTACAGCA CTTCCTTCGT CAAGGAGACC TTCGAAGAAC
-------------------------------------------------------------------------------

4701  AAGACAAACA ACGTCTGTAG CGACCCTTTG CAGGCAGCGG AACCCCCCAC
      TTCTGTTTGT TGCAGACATC GCTGGGAAAC GTCCGTCGCC TTGGGGGGTG
-------------------------------------------------------------------------------

4751  CTGGCGACAG GTGCCTCTGC GGCCAAAAGC CACGTGTATA AGATACACCT
      GACCGCTGTC CACGGAGACG CCGGTTTTCG GTGCACATAT TCTATGTGGA
-------------------------------------------------------------------------------
```

```
4801  GCAAAGGCGG CACAACCCCA GTGCCACGTT GTGAGTTGGA TAGTTGTGGA
      CGTTTCCGCC GTGTTGGGGT CACGGTGCAA CACTCAACCT ATCAACACCT

4851  AAGAGTCAAA TGGCTCTCCT CAAGCGTATT CAACAAGGGG CTGAAGGATG
      TTCTCAGTTT ACCGAGAGGA GTTCGCATAA GTTGTTCCCC GACTTCCTAC

4901  CCCAGAAGGT ACCCCATTGT ATGGGATCTG ATCTGGGGCC TCGGTGCACA
      GGGTCTTCCA TGGGGTAACA TACCCTAGAC TAGACCCCGG AGCCACGTGT

4951  TGCTTTACAT GTGTTTAGTC GAGGTTAAAA AACGTCTAGG CCCCCCGAAC
      ACGAAATGTA CACAAATCAG CTCCAATTTT TTGCAGATCC GGGGGGCTTG

5001  CACGGGGACG TGGTTTTCCT TTGAAAAACA CGATGATAAT ACCATGATTG
      GTGCCCCTGC ACCAAAAGGA AACTTTTTGT GCTACTATTA TGGTACTAAC

5051  AACAAGATGG ATTGCACGCA GGTTCTCCGG CCGCTTGGGT GGAGAGGCTA
      TTGTTCTACC TAACGTGCGT CCAAGAGGCC GGCGAACCCA CCTCTCCGAT

5101  TTCGGCTATG ACTGGGCACA ACAGACAATC GGCTGCTCTG ATGCCGCCGT
      AAGCCGATAC TGACCCGTGT TGTCTGTTAG CCGACGAGAC TACGGCGGCA

5151  GTTCCGGCTG TCAGCGCAGG GGCGCCCGGT TCTTTTTGTC AAGACCGACC
      CAAGGCCGAC AGTCGCGTCC CCGCGGGCCA AGAAAAACAG TTCTGGCTGG

5201  TGTCCGGTGC CCTGAATGAA CTGCAGGACG AGGCAGCGCG GCTATCGTGG
      ACAGGCCACG GGACTTACTT GACGTCCTGC TCCGTCGCGC CGATAGCACC

5251  CTGGCCACGA CGGGCGTTCC TTGCGCAGCT GTGCTCGACG TTGTCACTGA
      GACCGGTGCT GCCCGCAAGG AACGCGTCGA CACGAGCTGC AACAGTGACT

5301  AGCGGGAAGG GACTGGCTGC TATTGGGCGA AGTGCCGGGG CAGGATCTCC
      TCGCCCTTCC CTGACCGACG ATAACCCGCT TCACGGCCCC GTCCTAGAGG

5351  TGTCATCTCA CCTTGCTCCT GCCGAGAAAG TATCCATCAT GGCTGATGCA
      ACAGTAGAGT GGAACGAGGA CGGCTCTTTC ATAGGTAGTA CCGACTACGT

5401  ATGCGGCGGC TGCATACGCT TGATCCGGCT ACCTGCCCAT TCGACCACCA
      TACGCCGCCG ACGTATGCGA ACTAGGCCGA TGGACGGGTA AGCTGGTGGT

5451  AGCGAAACAT CGCATCGAGC GAGCACGTAC TCGGATGGAA GCCGGTCTTG
      TCGCTTTGTA GCGTAGCTCG CTCGTGCATG AGCCTACCTT CGGCCAGAAC

5501  TCGATCAGGA TGATCTGGAC GAAGAGCATC AGGGGCTCGC GCCAGCCGAA
      AGCTAGTCCT ACTAGACCTG CTTCTCGTAG TCCCCGAGCG CGGTCGGCTT

5551  CTGTTCGCCA GGCTCAAGGC GCGCATGCCC GACGGCGAGG ATCTCGTCGT
      GACAAGCGGT CCGAGTTCCG CGCGTACGGG CTGCCGCTCC TAGAGCAGCA

5601  GACCCATGGC GATGCCTGCT TGCCGAATAT CATGGTGGAA AATGGCCGCT
      CTGGGTACCG CTACGGACGA ACGGCTTATA GTACCACCTT TTACCGGCGA

5651  TTTCTGGATT CATCGACTGT GGCCGGCTGG GTGTGGCGGA CCGCTATCAG
      AAAGACCTAA GTAGCTGACA CCGGCCGACC CACACCGCCT GGCGATAGTC

5701  GACATAGCGT TGGCTACCCG TGATATTGCT GAAGAGCTTG GCGGCGAATG
      CTGTATCGCA ACCGATGGGC ACTATAACGA CTTCTCGAAC CGCCGCTTAC
```

```
5751  GGCTGACCGC TTCCTCGTGC TTTACGGTAT CGCCGCTCCC GATTCGCAGC
      CCGACTGGCG AAGGAGCACG AAATGCCATA GCGGCGAGGG CTAAGCGTCG

5801  GCATCGCCTT CTATCGCCTT CTTGACGAGT TCTTCTGAGC GGGACTCTGG
      CGTAGCGGAA GATAGCGGAA GAACTGCTCA AGAAGACTCG CCCTGAGACC

5851  GGTTCGCATC GATAAAATAA AAGATTTTAT TTAGTCTCCA GAAAAAGGGG
      CCAAGCGTAG CTATTTTATT TTCTAAAATA AATCAGAGGT CTTTTTCCCC

5901  GGAATGAAAG ACCCCACCTG TAGGTTTGGC AAGCTAGCTT AAGTAACGCC
      CCTTACTTTC TGGGGTGGAC ATCCAAACCG TTCGATCGAA TTCATTGCGG

5951  ATTTTGCAAG GCATGGAAAA ATACATAACT GAGAATAGAG AAGTTCAGAT
      TAAAACGTTC CGTACCTTTT TATGTATTGA CTCTTATCTC TTCAAGTCTA

6001  CAAGGTCAGG AACAGATGGA ACAGCTGAAT ATGGGCCAAA CAGGATATCT
      GTTCCAGTCC TTGTCTACCT TGTCGACTTA TACCCGGTTT GTCCTATAGA

6051  GTGGTAAGCA GTTCCTGCCC CGGCTCAGGG CCAAGAACAG ATGGAACAGC
      CACCATTCGT CAAGGACGGG GCCGAGTCCC GGTTCTTGTC TACCTTGTCG

6101  TGAATATGGG CCAAACAGGA TATCTGTGGT AAGCAGTTCC TGCCCCGGCT
      ACTTATACCC GGTTTGTCCT ATAGACACCA TTCGTCAAGG ACGGGGCCGA

6151  CAGGGCCAAG AACAGATGGT CCCCAGATGC GGTCCAGCCC TCAGCAGTTT
      GTCCCGGTTC TTGTCTACCA GGGGTCTACG CCAGGTCGGG AGTCGTCAAA

6201  CTAGAGAACC ATCAGATGTT TCCAGGGTGC CCCAAGGACC TGAAATGACC
      GATCTCTTGG TAGTCTACAA AGGTCCCACG GGGTTCCTGG ACTTTACTGG

6251  CTGTGCCTTA TTTGAACTAA CCAATCAGTT CGCTTCTCGC TTCTGTTCGC
      GACACGGAAT AAACTTGATT GGTTAGTCAA GCGAAGAGCG AAGACAAGCG

6301  GCGCTTCTGC TCCCCGAGCT CAATAAAAGA GCCCACAACC CCTCACTCGG
      CGCGAAGACG AGGGGCTCGA GTTATTTTCT CGGGTGTTGG GGAGTGAGCC

6351  GGCGCCAGTC CTCCGATTGA CTGAGTCGCC CGGGTACCCG TGTATCCAAT
      CCGCGGTCAG GAGGCTAACT GACTCAGCGG GCCCATGGGC ACATAGGTTA

6401  AAACCCTCTT GCAGTTGCAT CCGACTTGTG GTCTCGCTGT TCCTTGGGAG
      TTTGGGAGAA CGTCAACGTA GGCTGAACAC CAGAGCGACA AGGAACCCTC

6451  GGTCTCCTCT GAGTGATTGA CTACCCGTCA GCGGGGGTCT TTCATTCATG
      CCAGAGGAGA CTCACTAACT GATGGGCAGT CGCCCCCAGA AAGTAAGTAC

6501  CAGCATGTAT CAAAATTAAT TTGGTTTTTT TTCTTAAGTA TTTACATTAA
      GTCGTACATA GTTTTAATTA AACCAAAAAA AAGAATTCAT AAATGTAATT

6551  ATGGCCATAG TTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT
      TACCGGTATC AACGTAATTA CTTAGCCGGT TGCGCGCCCC TCTCCGCCAA

6601  TGCGTATTGG CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG
      ACGCATAACC GCGAGAAGGC GAAGGAGCGA GTGACTGAGC GACGCGAGCC

6651  TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG
      AGCAAGCCGA CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC
```

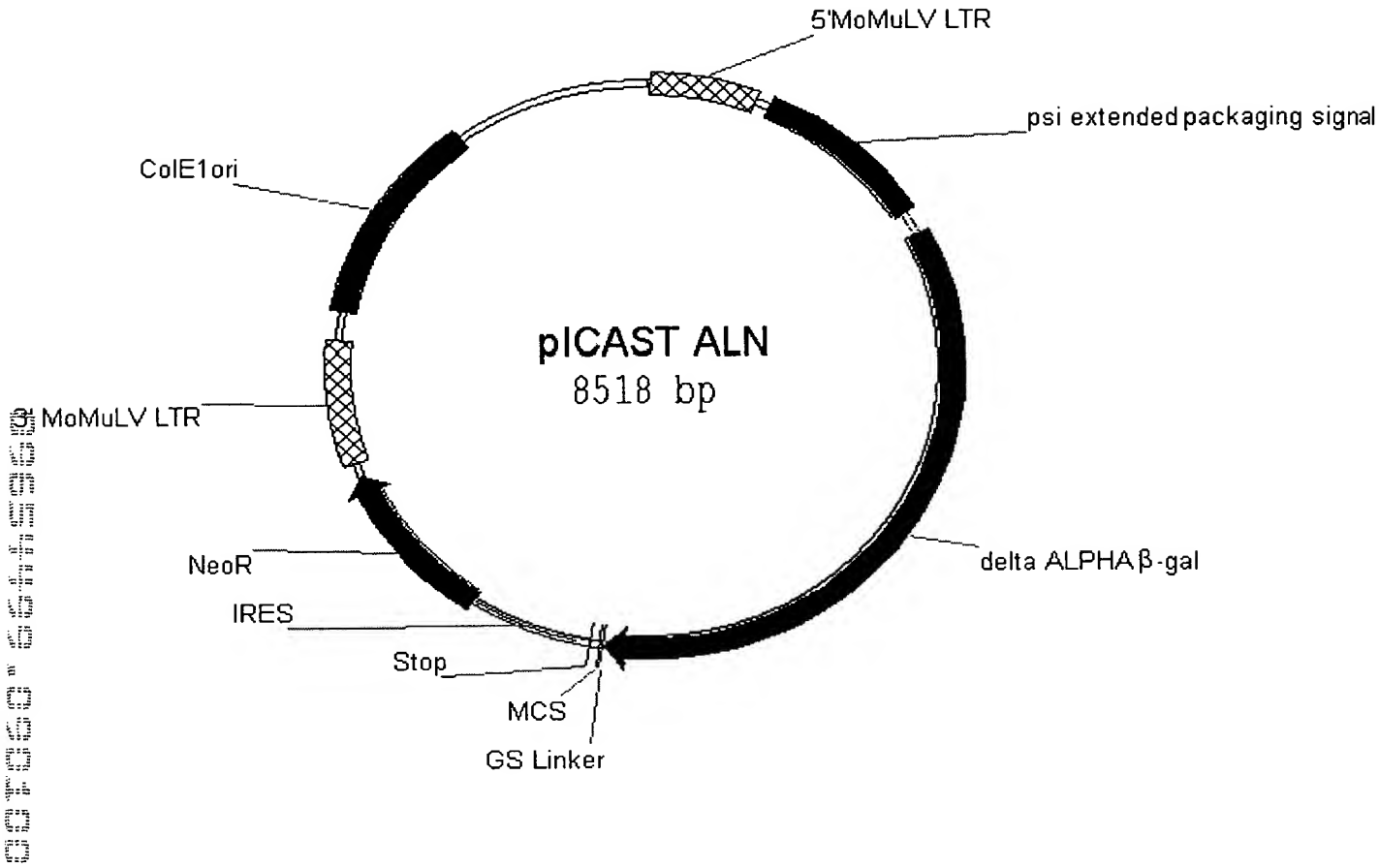
5'MoMuLV LTR
psi extended packaging signal
ColE1 ori
pICAST ALN
8518 bp
3' MoMuLV LTR
NeoR
IRES
Stop
MCS
GS Linker
delta ALPHA β-gal

Figure 11A

```
  1  CTGCAGCCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG
     GACGTCGGAC TTATACCCGG TTTGTCCTAT AGACACCATT CGTCAAGGAC
--------------------------------------------------------------------------------
 51  CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA
     GGGGCCGAGT CCCGGTTCTT GTCTACCTTG TCGACTTATA CCCGGTTTGT
--------------------------------------------------------------------------------
101  GGATATCTGT GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT
     CCTATAGACA CCATTCGTCA AGGACGGGGC CGAGTCCCGG TTCTTGTCTA
--------------------------------------------------------------------------------
151  GGTCCCCAGA TGCGGTCCAG CCCTCAGCAG TTTCTAGAGA ACCATCAGAT
     CCAGGGGTCT ACGCCAGGTC GGGAGTCGTC AAAGATCTCT TGGTAGTCTA
--------------------------------------------------------------------------------
201  GTTTCCAGGG TGCCCCAAGG ACCTGAAATG ACCCTGTGCC TTATTTGAAC
     CAAAGGTCCC ACGGGGTTCC TGGACTTTAC TGGGACACGG AATAAACTTG
--------------------------------------------------------------------------------
251  TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC TGCTCCCCGA
     ATTGGTTAGT CAAGCGAAGA GCGAAGACAA GCGCGCGAAG ACGAGGGGCT
--------------------------------------------------------------------------------
301  GCTCAATAAA AGAGCCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT
     CGAGTTATTT TCTCGGGTGT TGGGGAGTGA GCCCCGCGGT CAGGAGGCTA
--------------------------------------------------------------------------------
351  TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCCT CTTGCAGTTG
     ACTGACTCAG CGGGCCCATG GGCACATAGG TTATTTGGGA GAACGTCAAC
--------------------------------------------------------------------------------
401  CATCCGACTT GTGGTCTCGC TGTTCCTTGG GAGGGTCTCC TCTGAGTGAT
     GTAGGCTGAA CACCAGAGCG ACAAGGAACC CTCCCAGAGG AGACTCACTA
--------------------------------------------------------------------------------
451  TGACTACCCG TCAGCGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATCGG
     ACTGATGGGC AGTCGCCCCC AGAAAGTAAA CCCCCGAGCA GGCCCTAGCC
--------------------------------------------------------------------------------
501  GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG CAAGCTGGCC
     CTCTGGGGAC GGGTCCCTGG TGGCTGGGTG GTGGCCCTCC GTTCGACCGG
--------------------------------------------------------------------------------
551  AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG ACTGATTTTA
     TCGTTGAATA GACACAGACA GGCTAACAGA TCACAGATAC TGACTAAAAT
--------------------------------------------------------------------------------
601  TGCGCCTGCG TCGGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC
     ACGCGGACGC AGCCATGATC AATCGATTGA TCGAGACATA GACCGCCTGG
--------------------------------------------------------------------------------
651  CGTGGTGGAA CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG
     GCACCACCTT GACTGCTCAA GACTTGTGGG CCGGCGTTGG GACCCTCTGC
--------------------------------------------------------------------------------
701  TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG CCCGACCTGA GGAAGGGAGT
     AGGGTCCCTG AAACCCCCGG CAAAAACACC GGGCTGGACT CCTTCCCTCA
--------------------------------------------------------------------------------
751  CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
     GCTACACCTT AGGCTGGGGC AGTCCTATAC ACCAAGACCA TCCTCTGCTC
--------------------------------------------------------------------------------
801  AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA
     TTGGATTTTG TCAAGGGCGG AGGCAGACTT AAAAACGAAA GCCAAACCTT
--------------------------------------------------------------------------------
851  CCGAAGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT
     GGCTTCGGCG CGCAGAACAG ACGACGTCGT AGCAAGACAC AACAGAGACA
--------------------------------------------------------------------------------
901  CTGACTGTGT TTCTGTATTT GTCTGAAAAT TAGGGCCAGA CTGTTACCAC
     GACTGACACA AAGACATAAA CAGACTTTTA ATCCCGGTCT GACAATGGTG
--------------------------------------------------------------------------------
```

FIGURE 11B

```
 951  TCCCTTAAGT TTGACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG
-------------------------------------------------------------------------------
1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
-------------------------------------------------------------------------------
1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
-------------------------------------------------------------------------------
1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
-------------------------------------------------------------------------------
1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
-------------------------------------------------------------------------------
1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
-------------------------------------------------------------------------------
1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
-------------------------------------------------------------------------------
1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
-------------------------------------------------------------------------------
1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAACACCA
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTGTGGT
-------------------------------------------------------------------------------
1401  TGCACCATCA TCATCATCAC GTCGACTATA AAGATGAGGA CCTCGAGATG
      ACGTGGTAGT AGTAGTAGTG CAGCTGATAT TTCTACTCCT GGAGCTCTAC
-------------------------------------------------------------------------------
1451  GGCGTGATTA CGGATTCACT GGCCGTCGTG GCCCGCACCG ATCGCCCTTC
      CCGCACTAAT GCCTAAGTGA CCGGCAGCAC CGGGCGTGGC TAGCGGGAAG
-------------------------------------------------------------------------------
1501  CCAACAGTTA CGCAGCCTGA ATGGCGAATG GCGCTTTGCC TGGTTTCCGG
      GGTTGTCAAT GCGTCGGACT TACCGCTTAC CGCGAAACGG ACCAAAGGCC
-------------------------------------------------------------------------------
1551  CACCAGAAGC GGTGCCGGAA AGCTGGCTGG AGTGCGATCT TCCTGAGGCC
      GTGGTCTTCG CCACGGCCTT TCGACCGACC TCACGCTAGA AGGACTCCGG
-------------------------------------------------------------------------------
1601  GATACTGTCG TCGTCCCCTC AAACTGGCAG ATGCACGGTT ACGATGCGCC
      CTATGACAGC AGCAGGGGAG TTTGACCGTC TACGTGCCAA TGCTACGCGG
-------------------------------------------------------------------------------
1651  CATCTACACC AACGTGACCT ATCCCATTAC GGTCAATCCG CCGTTTGTTC
      GTAGATGTGG TTGCACTGGA TAGGGTAATG CCAGTTAGGC GGCAAACAAG
-------------------------------------------------------------------------------
1701  CCACGGAGAA TCCGACGGGT TGTTACTCGC TCACATTTAA TGTTGATGAA
      GGTGCCTCTT AGGCTGCCCA ACAATGAGCG AGTGTAAATT ACAACTACTT
-------------------------------------------------------------------------------
1751  AGCTGGCTAC AGGAAGGCCA GACGCGAATT ATTTTTGATG GCGTTAACTC
      TCGACCGATG TCCTTCCGGT CTGCGCTTAA TAAAAACTAC CGCAATTGAG
-------------------------------------------------------------------------------
1801  GGCGTTTCAT CTGTGGTGCA ACGGGCGCTG GGTCGGTTAC GGCCAGGACA
      CCGCAAAGTA GACACCACGT TGCCCGCGAC CCAGCCAATG CCGGTCCTGT
-------------------------------------------------------------------------------
1851  GTCGTTTGCC GTCTGAATTT GACCTGAGCG CATTTTTACG CGCCGGAGAA
      CAGCAAACGG CAGACTTAAA CTGGACTCGC GTAAAAATGC GCGGCCTCTT
-------------------------------------------------------------------------------
```

```
1901  AACCGCCTCG CGGTGATGGT GCTGCGCTGG AGTGACGGCA GTTATCTGGA
      TTGGCGGAGC GCCACTACCA CGACGCGACC TCACTGCCGT CAATAGACCT
-------------------------------------------------------------------------------
1951  AGATCAGGAT ATGTGGCGGA TGAGCGGCAT TTTCCGTGAC GTCTCGTTGC
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2001  TGCATAAACC GACTACACAA ATCAGCGATT TCCATGTTGC CACTCGCTTT
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      TTACTACTAA AGTCGGCGCG ACATGACCTC CGACTTCAAG TCTACACGCC
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2101  CGAGTTGCGT GACTACCTAC GGGTAACAGT TTCTTTATGG CAGGGTGAAA
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2151  CGCAGGTCGC CAGCGGCACC GCGCCTTTCG GCGGTGAAAT TATCGATGAG
      GCGTCCAGCG GTCGCCGTGG CGCGGAAAGC CGCCACTTTA ATAGCTACTC
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2201  CGTGGTGGTT ATGCCGATCG CGTCACACTA CGTCTGAACG TCGAAAACCC
      GCACCACCAA TACGGCTAGC GCAGTGTGAT GCAGACTTGC AGCTTTTGGG
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2251  GAAACTGTGG AGCGCCGAAA TCCCGAATCT CTATCGTGCG GTGGTTGAAC
      CTTTGACACC TCGCGGCTTT AGGGCTTAGA GATAGCACGC CACCAACTTG
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2301  TGCACACCGC CGACGGCACG CTGATTGAAG CAGAAGCCTG CGATGTCGGT
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2351  TTCCGCGAGG TGCGGATTGA AAATGGTCTG CTGCTGCTGA ACGGCAAGCC
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2401  GTTGCTGATT CGAGGCGTTA ACCGTCACGA GCATCATCCT CTGCATGGTC
      CAACGACTAA GCTCCGCAAT TGGCAGTGCT CGTAGTAGGA GACGTACCAG
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2451  AGGTCATGGA TGAGCAGACG ATGGTGCAGG ATATCCTGCT GATGAAGCAG
      TCCAGTACCT ACTCGTCTGC TACCACGTCC TATAGGACGA CTACTTCGTC
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2501  AACAACTTTA ACGCCGTGCG CTGTTCGCAT TATCCGAACC ATCCGCTGTG
      TTGTTGAAAT TGCGGCACGC GACAAGCGTA ATAGGCTTGG TAGGCGACAC
-------------------------------------------------------------------------------
2551  GTACACGCTG TGCGACCGCT ACGGCCTGTA TGTGGTGGAT GAAGCCAATA
      CATGTGCGAC ACGCTGGCGA TGCCGGACAT ACACCACCTA CTTCGGTTAT
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2601  TTGAAACCCA CGGCATGGTG CCAATGAATC GTCTGACCGA TGATCCGCGC
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2651  TGGCTACCGG CGATGAGCGA ACGCGTAACG CGAATGGTGC AGCGCGATCG
      ACCGATGGCC GCTACTCGCT TGCGCATTGC GCTTACCACG TCGCGCTAGC
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2701  TAATCACCCG AGTGTGATCA TCTGGTCGCT GGGGAATGAA TCAGGCCACG
      ATTAGTGGGC TCACACTAGT AGACCAGCGA CCCCTTACTT AGTCCGGTGC
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2751  GCGCTAATCA CGACGCGCTG TATCGCTGGA TCAAATCTGT CGATCCTTCC
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2801  CGCCCGGTGC AGTATGAAGG CGGCGGAGCC GACACCACGG CCACCGATAT
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2851  TATTTGCCCG ATGTACGCGC GCGTGGATGA AGACCAGCCC TTCCCGGCTG
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2901  TGCCGAAATG GTCCATCAAA AAATGGCTTT CGCTACCTGG AGAGACGCGC
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2951  CCGCTGATCC TTTGCGAATA CGCCCACGCG ATGGGTAACA GTCTTGGCGG
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3001  TTTCGCTAAA TACTGGCAGG CGTTTCGTCA GTATCCCCGT TTACAGGGCG
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3051  GCTTCGTCTG GGACTGGGTG GATCAGTCGC TGATTAAATA TGATGAAAAC
      CGAAGCAGAC CCTGACCCAC CTAGTCAGCG ACTAATTTAT ACTACTTTTG
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3101  GGCAACCCGT GGTCGGCTTA CGGCGGTGAT TTTGGCGATA CGCCGAACGA
      CCGTTGGGCA CCAGCCGAAT GCCGCCACTA AAACCGCTAT GCGGCTTGCT
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3151  TCGCCAGTTC TGTATGAACG GTCTGGTCTT TGCCGACCGC ACGCCGCATC
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3201  CAGCGCTGAC GGAAGCAAAA CACCAGCAGC AGTTTTTCCA GTTCCGTTTA
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3251  TCCGGGCAAA CCATCGAAGT GACCAGCGAA TACCTGTTCC GTCATAGCGA
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3351  GCGGTGAAGT GCCTCTGGAT GTCGCTCCAC AAGGTAAACA GTTGATTGAA
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3401  CTGCCTGAAC TACCGCAGCC GGAGAGCGCC GGGCAACTCT GGCTCACAGT
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3451  ACGCGTAGTG CAACCGAACG CGACCGCATG GTCAGAAGCC GGGCACATCA
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3501  GCGCCTGGCA GCAGTGGCGT CTGGCGGAAA ACCTCAGTGT GACGCTCCCC
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3551  GCCGCGTCCC ACGCCATCCC GCATCTGACC ACCAGCGAAA TGGATTTTTG
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3601  CATCGAGCTG GGTAATAAGC GTTGGCAATT TAACCGCCAG TCAGGCTTTC
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3651  TTTCACAGAT GTGGATTGGC GATAAAAAAC AACTGCTGAC GCCGCTGCGC
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3701  GATCAGTTCA CCCGTGCACC GCTGGATAAC GACATTGGCG TAAGTGAAGC
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3751  GACCCGCATT GACCCTAACG CCTGGGTCGA ACGCTGGAAG GCGGCGGGCC
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3851  GATGCGGTGC TGATTACGAC CGCTCACGCG TGGCAGCATC AGGGGAAAAC
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3901  CTTATTTATC AGCCGGAAAA CCTACCGGAT TGATGGTAGT GGTCAAATGG
      GAATAAATAG TCGGCCTTTT GGATGGCCTA ACTACCATCA CCAGTTTACC

3951  CGATTACCGT TGATGTTGAA GTGGCGAGCG ATACACCGCA TCCGGCGCGG
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4001  ATTGGCCTGA ACTGCCAGCT GGCGCAGGTA GCAGAGCGGG TAAACTGGCT
      TAACCGGACT TGACGGTCGA CCGCGTCCAT CGTCTCGCCC ATTTGACCGA

4051  CGGATTAGGG CCGCAAGAAA ACTATCCCGA CCGCCTTACT GCCGCCTGTT
      GCCTAATCCC GGCGTTCTTT TGATAGGGCT GGCGGAATGA CGGCGGACAA

4101  TTGACCGCTG GGATCTGCCA TTGTCAGACA TGTATACCCC GTACGTCTTC
      AACTGGCGAC CCTAGACGGT AACAGTCTGT ACATATGGGG CATGCAGAAG

4151  CCGAGCGAAA ACGGTCTGCG CTGCGGGACG CGCGAATTGA ATTATGGCCC
      GGCTCGCTTT TGCCAGACGC GACGCCCTGC GCGCTTAACT TAATACCGGG

4201  ACACCAGTGG CGCGGCGACT TCCAGTTCAA CATCAGCCGC TACAGTCAAC
      TGTGGTCACC GCGCCGCTGA AGGTCAAGTT GTAGTCGGCG ATGTCAGTTG

4251  AGCAACTGAT GGAAACCAGC CATCGCCATC TGCTGCACGC GGAAGAAGGC
      TCGTTGACTA CCTTTGGTCG GTAGCGGTAG ACGACGTGCG CCTTCTTCCG

4301  ACATGGCTGA ATATCGACGG TTTCCATATG GGGATTGGTG GCGACGACTC
      TGTACCGACT TATAGCTGCC AAAGGTATAC CCCTAACCAC CGCTGCTGAG

4351  CTGGAGCCCG TCAGTATCGG CGGAATTCCA GCTGAGCGCC GGTCGCTACC
      GACCTCGGGC AGTCATAGCC GCCTTAAGGT CGACTCGCGG CCAGCGATGG

4401  ATTACCAGTT GGTCTGGTGT CAAAAAAGAT CTGGAGGTGG TGGCAGCAGG
      TAATGGTCAA CCAGACCACA GTTTTTTCTA GACCTCCACC ACCGTCGTCC

4451  CCTTGGCGCG CCGGATCCTT AATTAACAAT TGACCGGTAA TAATAGGTAG
      GGAACCGCGC GGCCTAGGAA TTAATTGTTA ACTGGCCATT ATTATCCATC

4501  ATAAGTGACT GATTAGATGC ATTGATCCCT CGACCAATTC CGGTTATTTT
      TATTCACTGA CTAATCTACG TAACTAGGGA GCTGGTTAAG GCCAATAAAA

4551  CCACCATATT GCCGTCTTTT GGCAATGTGA GGGCCCGGAA ACCTGGCCCT
      GGTGGTATAA CGGCAGAAAA CCGTTACACT CCCGGGCCTT TGGACCGGGA

4601  GTCTTCTTGA CGAGCATTCC TAGGGGTCTT TCCCCTCTCG CCAAAGGAAT
      CAGAAGAACT GCTCGTAAGG ATCCCCAGAA AGGGGAGAGC GGTTTCCTTA

4651  GCAAGGTCTG TTGAATGTCG TGAAGGAAGC AGTTCCTCTG GAAGCTTCTT
      CGTTCCAGAC AACTTACAGC ACTTCCTTCG TCAAGGAGAC CTTCGAAGAA

4701  GAAGACAAAC AACGTCTGTA GCGACCCTTT GCAGGCAGCG GAACCCCCCA
      CTTCTGTTTG TTGCAGACAT CGCTGGGAAA CGTCCGTCGC CTTGGGGGGT
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4801  TGCAAAGGCG GCACAACCCC AGTGCCACGT TGTGAGTTGG ATAGTTGTGG
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4851  AAAGAGTCAA ATGGCTCTCC TCAAGCGTAT TCAACAAGGG GCTGAAGGAT
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5251  GCTGGCCACG ACGGGCGTTC CTTGCGCAGC TGTGCTCGAC GTTGTCACTG
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5301  AAGCGGGAAG GGACTGGCTG CTATTGGGCG AAGTGCCGGG GCAGGATCTC
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5351  CTGTCATCTC ACCTTGCTCC TGCCGAGAAA GTATCCATCA TGGCTGATGC
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5401  AATGCGGCGG CTGCATACGC TTGATCCGGC TACCTGCCCA TTCGACCACC
      TTACGCCGCC GACGTATGCG AACTAGGCCG ATGGACGGGT AAGCTGGTGG
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5451  AAGCGAAACA TCGCATCGAG CGAGCACGTA CTCGGATGGA AGCCGGTCTT
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5501  GTCGATCAGG ATGATCTGGA CGAAGAGCAT CAGGGGCTCG CGCCAGCCGA
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5601  TGACCCATGG CGATGCCTGC TTGCCGAATA TCATGGTGGA AAATGGCCGC
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6251  CCTGTGCCTT ATTTGAACTA ACCAATCAGT TCGCTTCTCG CTTCTGTTCG
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6351  GGGCGCCAGT CCTCCGATTG ACTGAGTCGC CCGGGTACCC GTGTATCCAA
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6451  GGGTCTCCTC TGAGTGATTG ACTACCCGTC AGCGGGGGTC TTTCATTCAT
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7201  TCTTGAAGTG GTGGCCTAAC TACGGCTACA CTAGAAGAAC AGTATTTGGT
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7251  ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
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8251  CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC
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8301  TTCAGCATCT TTTACTTTCA CCAGCGTTTC TGGGTGAGCA AAAACAGGAA
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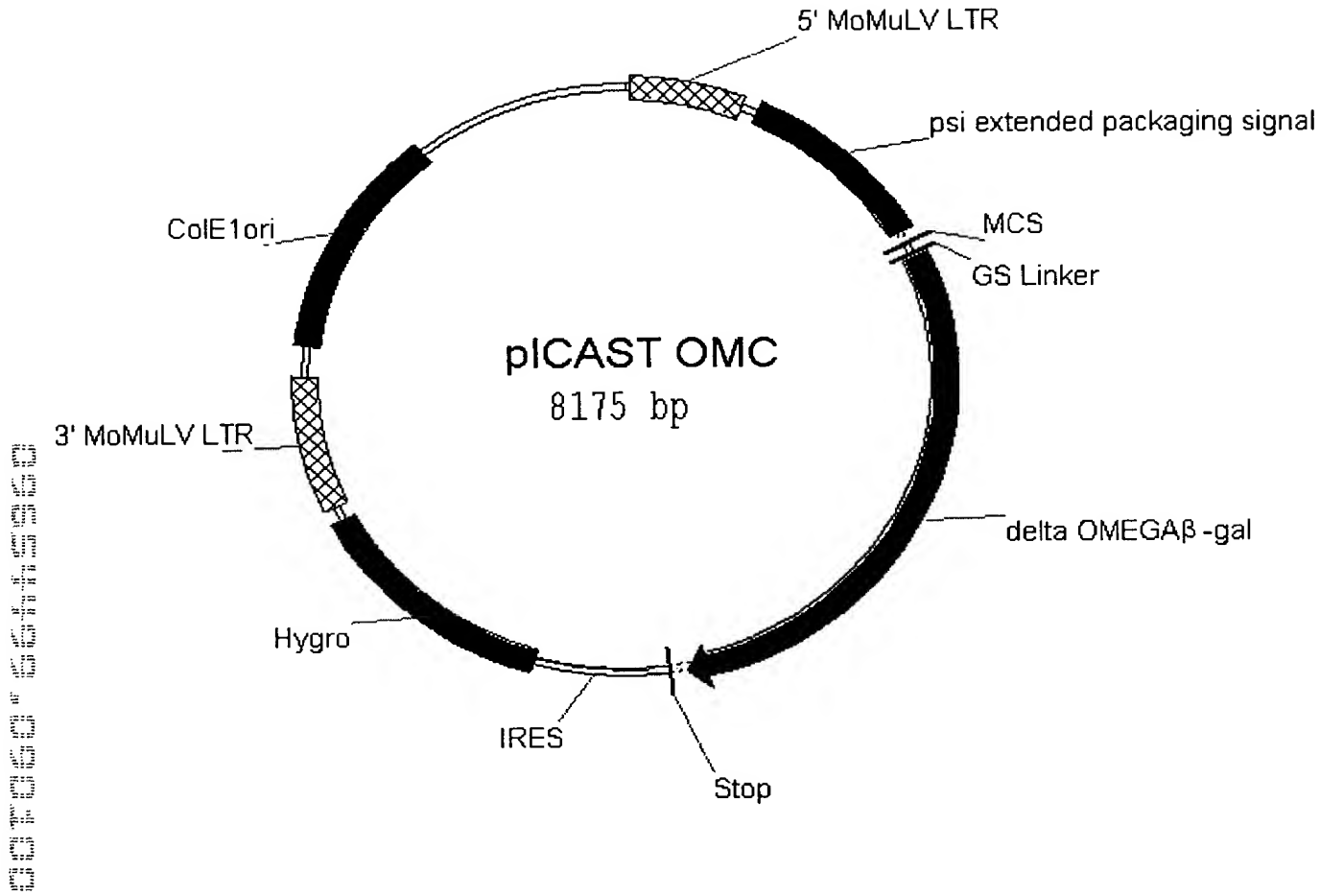
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Hygro
3' MoMuLV LTR
ColE1ori
pICAST OMC
8175 bp

Figure 12A

```
  1  CTGCAGCCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG
     GACGTCGGAC TTATACCCGG TTTGTCCTAT AGACACCATT CGTCAAGGAC
---------------------------------------------------------------------------
 51  CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA
     GGGGCCGAGT CCCGGTTCTT GTCTACCTTG TCGACTTATA CCCGGTTTGT
---------------------------------------------------------------------------
101  GGATATCTGT GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT
     CCTATAGACA CCATTCGTCA AGGACGGGGC CGAGTCCCGG TTCTTGTCTA
---------------------------------------------------------------------------
151  GGTCCCCAGA TGCGGTCCAG CCCTCAGCAG TTTCTAGAGA ACCATCAGAT
     CCAGGGGTCT ACGCCAGGTC GGGAGTCGTC AAAGATCTCT TGGTAGTCTA
---------------------------------------------------------------------------
201  GTTTCCAGGG TGCCCCAAGG ACCTGAAATG ACCCTGTGCC TTATTTGAAC
     CAAAGGTCCC ACGGGGTTCC TGGACTTTAC TGGGACACGG AATAAACTTG
---------------------------------------------------------------------------
251  TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC TGCTCCCCGA
     ATTGGTTAGT CAAGCGAAGA GCGAAGACAA GCGCGCGAAG ACGAGGGGCT
---------------------------------------------------------------------------
301  GCTCAATAAA AGAGCCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT
     CGAGTTATTT TCTCGGGTGT TGGGGAGTGA GCCCCGCGGT CAGGAGGCTA
---------------------------------------------------------------------------
351  TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCCT CTTGCAGTTG
     ACTGACTCAG CGGGCCCATG GGCACATAGG TTATTTGGGA GAACGTCAAC
---------------------------------------------------------------------------
401  CATCCGACTT GTGGTCTCGC TGTTCCTTGG GAGGGTCTCC TCTGAGTGAT
     GTAGGCTGAA CACCAGAGCG ACAAGGAACC CTCCCAGAGG AGACTCACTA
---------------------------------------------------------------------------
451  TGACTACCCG TCAGCGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATCGG
     ACTGATGGGC AGTCGCCCCC AGAAAGTAAA CCCCCGAGCA GGCCCTAGCC
---------------------------------------------------------------------------
501  GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG CAAGCTGGCC
     CTCTGGGGAC GGGTCCCTGG TGGCTGGGTG GTGGCCCTCC GTTCGACCGG
---------------------------------------------------------------------------
551  AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG ACTGATTTTA
     TCGTTGAATA GACACAGACA GGCTAACAGA TCACAGATAC TGACTAAAAT
---------------------------------------------------------------------------
601  TGCGCCTGCG TCGGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC
     ACGCGGACGC AGCCATGATC AATCGATTGA TCGAGACATA GACCGCCTGG
---------------------------------------------------------------------------
651  CGTGGTGGAA CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG
     GCACCACCTT GACTGCTCAA GACTTGTGGG CCGGCGTTGG GACCCTCTGC
---------------------------------------------------------------------------
701  TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG CCCGACCTGA GGAAGGGAGT
     AGGGTCCCTG AAACCCCCGG CAAAAACACC GGGCTGGACT CCTTCCCTCA
---------------------------------------------------------------------------
751  CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
     GCTACACCTT AGGCTGGGGC AGTCCTATAC ACCAAGACCA TCCTCTGCTC
---------------------------------------------------------------------------
801  AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA
     TTGGATTTTG TCAAGGGCGG AGGCAGACTT AAAAACGAAA GCCAAACCTT
---------------------------------------------------------------------------
851  CCGAAGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT
     GGCTTCGGCG CGCAGAACAG ACGACGTCGT AGCAAGACAC AACAGAGACA
---------------------------------------------------------------------------
901  CTGACTGTGT TTCTGTATTT GTCTGAAAAT TAGGGCCAGA CTGTTACCAC
     GACTGACACA AAGACATAAA CAGACTTTTA ATCCCGGTCT GACAATGGTG
---------------------------------------------------------------------------
```

FIGURE 12B

```
 951  TCCCTTAAGT TTGACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG
------------------------------------------------------------------------------
1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
------------------------------------------------------------------------------
1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
------------------------------------------------------------------------------
1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
------------------------------------------------------------------------------
1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
------------------------------------------------------------------------------
1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
------------------------------------------------------------------------------
1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
------------------------------------------------------------------------------
1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
------------------------------------------------------------------------------
1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAATCAGG
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTAGTCC
------------------------------------------------------------------------------
1401  CCTTGGCGCG CCGGATCCTT AATTAAGCGC AATTGGGAGG TGGCGGTAGC
      GGAACCGCGC GGCCTAGGAA TTAATTCGCG TTAACCCTCC ACCGCCATCG
------------------------------------------------------------------------------
1451  CTCGAGATGG GCGTGATTAC GGATTCACTG GCCGTCGTTT TACAACGTCG
      GAGCTCTACC CGCACTAATG CCTAAGTGAC CGGCAGCAAA ATGTTGCAGC
------------------------------------------------------------------------------
1501  TGACTGGGAA AACCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC
      ACTGACCCTT TTGGGACCGC AATGGGTTGA ATTAGCGGAA CGTCGTGTAG
------------------------------------------------------------------------------
1551  CCCCTTTCGC CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATCGCCCT
      GGGGAAAGCG GTCGACCGCA TTATCGCTTC TCCGGGCGTG GCTAGCGGGA
------------------------------------------------------------------------------
1601  TCCCAACAGT TACGCAGCCT GAATGGCGAA TGGCGCTTTG CCTGGTTTCC
      AGGGTTGTCA ATGCGTCGGA CTTACCGCTT ACCGCGAAAC GGACCAAAGG
------------------------------------------------------------------------------
1651  GGCACCAGAA GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT CTTCCTGAGG
      CCGTGGTCTT CGCCACGGCC TTTCGACCGA CCTCACGCTA GAAGGACTCC
------------------------------------------------------------------------------
1701  CCGATACTGT CGTCGTCCCC TCAAACTGGC AGATGCACGG TTACGATGCG
      GGCTATGACA GCAGCAGGGG AGTTTGACCG TCTACGTGCC AATGCTACGC
------------------------------------------------------------------------------
1751  CCCATCTACA CCAACGTGAC CTATCCCATT ACGGTCAATC CGCCGTTTGT
      GGGTAGATGT GGTTGCACTG GATAGGGTAA TGCCAGTTAG GCGGCAAACA
------------------------------------------------------------------------------
1801  TCCCACGGAG AATCCGACGG GTTGTTACTC GCTCACATTT AATGTTGATG
      AGGGTGCCTC TTAGGCTGCC CAACAATGAG CGAGTGTAAA TTACAACTAC
------------------------------------------------------------------------------
1851  AAAGCTGGCT ACAGGAAGGC CAGACGCGAA TTATTTTTGA TGGCGTTAAC
      TTTCGACCGA TGTCCTTCCG GTCTGCGCTT AATAAAAACT ACCGCAATTG
------------------------------------------------------------------------------
```

```
1901  TCGGCGTTTC ATCTGTGGTG CAACGGGCGC TGGGTCGGTT ACGGCCAGGA
      AGCCGCAAAG TAGACACCAC GTTGCCCGCG ACCCAGCCAA TGCCGGTCCT
-------------------------------------------------------------------------------
1951  CAGTCGTTTG CCGTCTGAAT TTGACCTGAG CGCATTTTTA CGCGCCGGAG
      GTCAGCAAAC GGCAGACTTA AACTGGACTC GCGTAAAAAT GCGCGGCCTC
-------------------------------------------------------------------------------
2001  AAAACCGCCT CGCGGTGATG GTGCTGCGCT GGAGTGACGG CAGTTATCTG
      TTTTGGCGGA GCGCCACTAC CACGACGCGA CCTCACTGCC GTCAATAGAC
-------------------------------------------------------------------------------
2051  GAAGATCAGG ATATGTGGCG GATGAGCGGC ATTTTCCGTG ACGTCTCGTT
      CTTCTAGTCC TATACACCGC CTACTCGCCG TAAAAGGCAC TGCAGAGCAA
-------------------------------------------------------------------------------
2101  GCTGCATAAA CCGACTACAC AAATCAGCGA TTTCCATGTT GCCACTCGCT
      CGACGTATTT GGCTGATGTG TTTAGTCGCT AAAGGTACAA CGGTGAGCGA
-------------------------------------------------------------------------------
2151  TTAATGATGA TTTCAGCCGC GCTGTACTGG AGGCTGAAGT TCAGATGTGC
      AATTACTACT AAAGTCGGCG CGACATGACC TCCGACTTCA AGTCTACACG
-------------------------------------------------------------------------------
2201  GGCGAGTTGC GTGACTACCT ACGGGTAACA GTTTCTTTAT GGCAGGGTGA
      CCGCTCAACG CACTGATGGA TGCCCATTGT CAAAGAAATA CCGTCCCACT
-------------------------------------------------------------------------------
2251  AACGCAGGTC GCCAGCGGCA CCGCGCCTTT CGGCGGTGAA ATTATCGATG
      TTGCGTCCAG CGGTCGCCGT GGCGCGGAAA GCCGCCACTT TAATAGCTAC
-------------------------------------------------------------------------------
2301  AGCGTGGTGG TTATGCCGAT CGCGTCACAC TACGTCTGAA CGTCGAAAAC
      TCGCACCACC AATACGGCTA GCGCAGTGTG ATGCAGACTT GCAGCTTTTG
-------------------------------------------------------------------------------
2351  CCGAAACTGT GGAGCGCCGA AATCCCGAAT CTCTATCGTG CGGTGGTTGA
      GGCTTTGACA CCTCGCGGCT TTAGGGCTTA GAGATAGCAC GCCACCAACT
-------------------------------------------------------------------------------
2401  ACTGCACACC GCCGACGGCA CGCTGATTGA AGCAGAAGCC TGCGATGTCG
      TGACGTGTGG CGGCTGCCGT GCGACTAACT TCGTCTTCGG ACGCTACAGC
-------------------------------------------------------------------------------
2451  GTTTCCGCGA GGTGCGGATT GAAAATGGTC TGCTGCTGCT GAACGGCAAG
      CAAAGGCGCT CCACGCCTAA CTTTTACCAG ACGACGACGA CTTGCCGTTC
-------------------------------------------------------------------------------
2501  CCGTTGCTGA TTCGAGGCGT TAACCGTCAC GAGCATCATC CTCTGCATGG
      GGCAACGACT AAGCTCCGCA ATTGGCAGTG CTCGTAGTAG GAGACGTACC
-------------------------------------------------------------------------------
2551  TCAGGTCATG GATGAGCAGA CGATGGTGCA GGATATCCTG CTGATGAAGC
      AGTCCAGTAC CTACTCGTCT GCTACCACGT CCTATAGGAC GACTACTTCG
-------------------------------------------------------------------------------
2601  AGAACAACTT TAACGCCGTG CGCTGTTCGC ATTATCCGAA CCATCCGCTG
      TCTTGTTGAA ATTGCGGCAC GCGACAAGCG TAATAGGCTT GGTAGGCGAC
-------------------------------------------------------------------------------
2651  TGGTACACGC TGTGCGACCG CTACGGCCTG TATGTGGTGG ATGAAGCCAA
      ACCATGTGCG ACACGCTGGC GATGCCGGAC ATACACCACC TACTTCGGTT
-------------------------------------------------------------------------------
2701  TATTGAAACC CACGGCATGG TGCCAATGAA TCGTCTGACC GATGATCCGC
      ATAACTTTGG GTGCCGTACC ACGGTTACTT AGCAGACTGG CTACTAGGCG
-------------------------------------------------------------------------------
2751  GCTGGCTACC GGCGATGAGC GAACGCGTAA CGCGAATGGT GCAGCGCGAT
      CGACCGATGG CCGCTACTCG CTTGCGCATT GCGCTTACCA CGTCGCGCTA
-------------------------------------------------------------------------------
2801  CGTAATCACC CGAGTGTGAT CATCTGGTCG CTGGGGAATG AATCAGGCCA
      GCATTAGTGG GCTCACACTA GTAGACCAGC GACCCCTTAC TTAGTCCGGT
-------------------------------------------------------------------------------
```

```
2851  CGGCGCTAAT CACGACGCGC TGTATCGCTG GATCAAATCT GTCGATCCTT
      GCCGCGATTA GTGCTGCGCG ACATAGCGAC CTAGTTTAGA CAGCTAGGAA
-------------------------------------------------------------------------------
2901  CCCGCCCGGT GCAGTATGAA GGCGGCGGAG CCGACACCAC GGCCACCGAT
      GGGCGGGCCA CGTCATACTT CCGCCGCCTC GGCTGTGGTG CCGGTGGCTA
-------------------------------------------------------------------------------
2951  ATTATTTGCC CGATGTACGC GCGCGTGGAT GAAGACCAGC CCTTCCCGGC
      TAATAAACGG GCTACATGCG CGCGCACCTA CTTCTGGTCG GGAAGGGCCG
-------------------------------------------------------------------------------
3001  TGTGCCGAAA TGGTCCATCA AAAAATGGCT TTCGCTACCT GGAGAGACGC
      ACACGGCTTT ACCAGGTAGT TTTTTACCGA AAGCGATGGA CCTCTCTGCG
-------------------------------------------------------------------------------
3051  GCCCGCTGAT CCTTTGCGAA TACGCCCACG CGATGGGTAA CAGTCTTGGC
      CGGGCGACTA GGAAACGCTT ATGCGGGTGC GCTACCCATT GTCAGAACCG
-------------------------------------------------------------------------------
3101  GGTTTCGCTA AATACTGGCA GGCGTTTCGT CAGTATCCCC GTTTACAGGG
      CCAAAGCGAT TTATGACCGT CCGCAAAGCA GTCATAGGGG CAAATGTCCC
-------------------------------------------------------------------------------
3151  CGGCTTCGTC TGGGACTGGG TGGATCAGTC GCTGATTAAA TATGATGAAA
      GCCGAAGCAG ACCCTGACCC ACCTAGTCAG CGACTAATTT ATACTACTTT
-------------------------------------------------------------------------------
3201  ACGGCAACCC GTGGTCGGCT TACGGCGGTG ATTTTGGCGA TACGCCGAAC
      TGCCGTTGGG CACCAGCCGA ATGCCGCCAC TAAAACCGCT ATGCGGCTTG
-------------------------------------------------------------------------------
3251  GATCGCCAGT TCTGTATGAA CGGTCTGGTC TTTGCCGACC GCACGCCGCA
      CTAGCGGTCA AGACATACTT GCCAGACCAG AAACGGCTGG CGTGCGGCGT
-------------------------------------------------------------------------------
3301  TCCAGCGCTG ACGGAAGCAA AACACCAGCA GCAGTTTTTC CAGTTCCGTT
      AGGTCGCGAC TGCCTTCGTT TTGTGGTCGT CGTCAAAAAG GTCAAGGCAA
-------------------------------------------------------------------------------
3351  TATCCGGGCA AACCATCGAA GTGACCAGCG AATACCTGTT CCGTCATAGC
      ATAGGCCCGT TTGGTAGCTT CACTGGTCGC TTATGGACAA GGCAGTATCG
-------------------------------------------------------------------------------
3401  GATAACGAGC TCCTGCACTG GATGGTGGCG CTGGATGGTA AGCCGCTGGC
      CTATTGCTCG AGGACGTGAC CTACCACCGC GACCTACCAT TCGGCGACCG
-------------------------------------------------------------------------------
3451  AAGCGGTGAA GTGCCTCTGG ATGTCGCTCC ACAAGGTAAA CAGTTGATTG
      TTCGCCACTT CACGGAGACC TACAGCGAGG TGTTCCATTT GTCAACTAAC
-------------------------------------------------------------------------------
3501  AACTGCCTGA ACTACCGCAG CCGGAGAGCG CCGGGCAACT CTGGCTCACA
      TTGACGGACT TGATGGCGTC GGCCTCTCGC GGCCCGTTGA GACCGAGTGT
-------------------------------------------------------------------------------
3551  GTACGCGTAG TGCAACCGAA CGCGACCGCA TGGTCAGAAG CCGGGCACAT
      CATGCGCATC ACGTTGGCTT GCGCTGGCGT ACCAGTCTTC GGCCCGTGTA
-------------------------------------------------------------------------------
3601  CAGCGCCTGG CAGCAGTGGC GTCTGGCGGA AAACCTCAGT GTGACGCTCC
      GTCGCGGACC GTCGTCACCG CAGACCGCCT TTTGGAGTCA CACTGCGAGG
-------------------------------------------------------------------------------
3651  CCGCCGCGTC CCACGCCATC CCGCATCTGA CCACCAGCGA AATGGATTTT
      GGCGGCGCAG GGTGCGGTAG GGCGTAGACT GGTGGTCGCT TTACCTAAAA
-------------------------------------------------------------------------------
3701  TGCATCGAGC TGGGTAATAA GCGTTGGCAA TTTAACCGCC AGTCAGGCTT
      ACGTAGCTCG ACCCATTATT CGCAACCGTT AAATTGGCGG TCAGTCCGAA
-------------------------------------------------------------------------------
3751  TCTTTCACAG ATGTGGATTG GCGATAAAAA ACAACTGCTG ACGCCGCTGC
      AGAAAGTGTC TACACCTAAC CGCTATTTTT TGTTGACGAC TGCGGCGACG
-------------------------------------------------------------------------------
```

```
3801  GCGATCAGTT CACCCGTGTC GATAGATCTG AACAGAAACT CATTTCCGAA
      CGCTAGTCAA GTGGGCACAG CTATCTAGAC TTGTCTTTGA GTAAAGGCTT
-------------------------------------------------------------------------------
3851  GAAGACCTAG TCGACCATCA TCATCATCAT CACCGGTAAT AATAGGTAGA
      CTTCTGGATC AGCTGGTAGT AGTAGTAGTA GTGGCCATTA TTATCCATCT
-------------------------------------------------------------------------------
3901  TAAGTGACTG ATTAGATGCA TTTCGACTAG ATCCCTCGAC CAATTCCGGT
      ATTCACTGAC TAATCTACGT AAAGCTGATC TAGGGAGCTG GTTAAGGCCA
-------------------------------------------------------------------------------
3951  TATTTTCCAC CATATTGCCG TCTTTTGGCA ATGTGAGGGC CCGGAAACCT
      ATAAAAGGTG GTATAACGGC AGAAAACCGT TACACTCCCG GGCCTTTGGA
-------------------------------------------------------------------------------
4001  GGCCCTGTCT TCTTGACGAG CATTCCTAGG GGTCTTTCCC CTCTCGCCAA
      CCGGGACAGA AGAACTGCTC GTAAGGATCC CCAGAAAGGG GAGAGCGGTT
-------------------------------------------------------------------------------
4051  AGGAATGCAA GGTCTGTTGA ATGTCGTGAA GGAAGCAGTT CCTCTGGAAG
      TCCTTACGTT CCAGACAACT TACAGCACTT CCTTCGTCAA GGAGACCTTC
-------------------------------------------------------------------------------
4101  CTTCTTGAAG ACAAACAACG TCTGTAGCGA CCCTTTGCAG GCAGCGGAAC
      GAAGAACTTC TGTTTGTTGC AGACATCGCT GGGAAACGTC CGTCGCCTTG
-------------------------------------------------------------------------------
4151  CCCCCACCTG GCGACAGGTG CCTCTGCGGC CAAAAGCCAC GTGTATAAGA
      GGGGGTGGAC CGCTGTCCAC GGAGACGCCG GTTTTCGGTG CACATATTCT
-------------------------------------------------------------------------------
4201  TACACCTGCA AAGGCGGCAC AACCCCAGTG CCACGTTGTG AGTTGGATAG
      ATGTGGACGT TTCCGCCGTG TTGGGGTCAC GGTGCAACAC TCAACCTATC
-------------------------------------------------------------------------------
4251  TTGTGGAAAG AGTCAAATGG CTCTCCTCAA GCGTATTCAA CAAGGGGCTG
      AACACCTTTC TCAGTTTACC GAGAGGAGTT CGCATAAGTT GTTCCCCGAC
-------------------------------------------------------------------------------
4301  AAGGATGCCC AGAAGGTACC CCATTGTATG GGATCTGATC TGGGGCCTCG
      TTCCTACGGG TCTTCCATGG GGTAACATAC CCTAGACTAG ACCCCGGAGC
-------------------------------------------------------------------------------
4351  GTGCACATGC TTTACATGTG TTTAGTCGAG GTTAAAAAAC GTCTAGGCCC
      CACGTGTACG AAATGTACAC AAATCAGCTC CAATTTTTTG CAGATCCGGG
-------------------------------------------------------------------------------
4401  CCCGAACCAC GGGGACGTGG TTTTCCTTTG AAAAACACGA TGATAATACC
      GGGCTTGGTG CCCCTGCACC AAAAGGAAAC TTTTTGTGCT ACTATTATGG
-------------------------------------------------------------------------------
4451  ATGAAAAAGC CTGAACTCAC CGCGACGTCT GTCGAGAAGT TTCTGATCGA
      TACTTTTTCG GACTTGAGTG GCGCTGCAGA CAGCTCTTCA AAGACTAGCT
-------------------------------------------------------------------------------
4501  AAAGTTCGAC AGCGTCTCCG ACCTGATGCA GCTCTCGGAG GGCGAAGAAT
      TTTCAAGCTG TCGCAGAGGC TGGACTACGT CGAGAGCCTC CCGCTTCTTA
-------------------------------------------------------------------------------
4551  CTCGTGCTTT CAGCTTCGAT GTAGGAGGGC GTGGATATGT CCTGCGGGTA
      GAGCACGAAA GTCGAAGCTA CATCCTCCCG CACCTATACA GGACGCCCAT
-------------------------------------------------------------------------------
4601  AATAGCTGCG CCGATGGTTT CTACAAAGAT CGTTATGTTT ATCGGCACTT
      TTATCGACGC GGCTACCAAA GATGTTTCTA GCAATACAAA TAGCCGTGAA
-------------------------------------------------------------------------------
4651  TGCATCGGCC GCGCTCCCGA TTCCGGAAGT GCTTGACATT GGGGAATTTA
      ACGTAGCCGG CGCGAGGGCT AAGGCCTTCA CGAACTGTAA CCCCTTAAAT
-------------------------------------------------------------------------------
4701  GCGAGAGCCT GACCTATTGC ATCTCCCGCC GTGCACAGGG TGTCACGTTG
      CGCTCTCGGA CTGGATAACG TAGAGGGCGG CACGTGTCCC ACAGTGCAAC
-------------------------------------------------------------------------------
```

```
4751  CAAGACCTGC CTGAAACCGA ACTGCCCGCT GTTCTGCAGC CGGTCGCGGA
      GTTCTGGACG GACTTTGGCT TGACGGGCGA CAAGACGTCG GCCAGCGCCT

4801  GGCCATGGAT GCGATCGCTG CGGCCGATCT TAGCCAGACG AGCGGGTTCG
      CCGGTACCTA CGCTAGCGAC GCCGGCTAGA ATCGGTCTGC TCGCCCAAGC

4851  GCCCATTCGG ACCGCAAGGA ATCGGTCAAT ACACTACATG GCGTGATTTC
      CGGGTAAGCC TGGCGTTCCT TAGCCAGTTA TGTGATGTAC CGCACTAAAG

4901  ATATGCGCGA TTGCTGATCC CCATGTGTAT CACTGGCAAA CTGTGATGGA
      TATACGCGCT AACGACTAGG GGTACACATA GTGACCGTTT GACACTACCT

4951  CGACACCGTC AGTGCGTCCG TCGCGCAGGC TCTCGATGAG CTGATGCTTT
      GCTGTGGCAG TCACGCAGGC AGCGCGTCCG AGAGCTACTC GACTACGAAA

5001  GGGCCGAGGA CTGCCCCGAA GTCCGGCACC TCGTGCACGC GGATTTCGGC
      CCCGGCTCCT GACGGGGCTT CAGGCCGTGG AGCACGTGCG CCTAAAGCCG

5051  TCCAACAATG TCCTGACGGA CAATGGCCGC ATAACAGCGG TCATTGACTG
      AGGTTGTTAC AGGACTGCCT GTTACCGGCG TATTGTCGCC AGTAACTGAC

5101  GAGCGAGGCG ATGTTCGGGG ATTCCCAATA CGAGGTCGCC AACATCTTCT
      CTCGCTCCGC TACAAGCCCC TAAGGGTTAT GCTCCAGCGG TTGTAGAAGA

5151  TCTGGAGGCC GTGGTTGGCT TGTATGGAGC AGCAGACGCG CTACTTCGAG
      AGACCTCCGG CACCAACCGA ACATACCTCG TCGTCTGCGC GATGAAGCTC

5201  CGGAGGCATC CGGAGCTTGC AGGATCGCCG CGGCTCCGGG CGTATATGCT
      GCCTCCGTAG GCCTCGAACG TCCTAGCGGC GCCGAGGCCC GCATATACGA

5251  CCGCATTGGT CTTGACCAAC TCTATCAGAG CTTGGTTGAC GGCAATTTCG
      GGCGTAACCA GAACTGGTTG AGATAGTCTC GAACCAACTG CCGTTAAAGC

5301  ATGATGCAGC TTGGGCGCAG GGTCGATGCG ACGCAATCGT CCGATCCGGA
      TACTACGTCG AACCCGCGTC CCAGCTACGC TGCGTTAGCA GGCTAGGCCT

5351  GCCGGGACTG TCGGGCGTAC ACAAATCGCC CGCAGAAGCG CGGCCGTCTG
      CGGCCCTGAC AGCCCGCATG TGTTTAGCGG GCGTCTTCGC GCCGGCAGAC

5401  GACCGATGGC TGTGTAGAAG TACTCGCCGA TAGTGGAAAC CGACGCCCCA
      CTGGCTACCG ACACATCTTC ATGAGCGGCT ATCACCTTTG GCTGCGGGGT

5451  GCACTCGTCC GAGGGCAAAG GAATAGAGTA GATGCCGACC GGGATCTATC
      CGTGAGCAGG CTCCCGTTTC CTTATCTCAT CTACGGCTGG CCCTAGATAG

5501  GATAAAATAA AAGATTTTAT TTAGTCTCCA GAAAAAGGGG GGAATGAAAG
      CTATTTTATT TTCTAAAATA AATCAGAGGT CTTTTTCCCC CCTTACTTTC

5551  ACCCCACCTG TAGGTTTGGC AAGCTAGCTT AAGTAACGCC ATTTTGCAAG
      TGGGGTGGAC ATCCAAACCG TTCGATCGAA TTCATTGCGG TAAAACGTTC

5601  GCATGGAAAA ATACATAACT GAGAATAGAG AAGTTCAGAT CAAGGTCAGG
      CGTACCTTTT TATGTATTGA CTCTTATCTC TTCAAGTCTA GTTCCAGTCC

5651  AACAGATGGA ACAGCTGAAT ATGGGCCAAA CAGGATATCT GTGGTAAGCA
      TTGTCTACCT TGTCGACTTA TACCCGGTTT GTCCTATAGA CACCATTCGT
```

```
5701  GTTCCTGCCC CGGCTCAGGG CCAAGAACAG ATGGAACAGC TGAATATGGG
      CAAGGACGGG GCCGAGTCCC GGTTCTTGTC TACCTTGTCG ACTTATACCC
-------------------------------------------------------------------------------
5751  CCAAACAGGA TATCTGTGGT AAGCAGTTCC TGCCCCGGCT CAGGGCCAAG
      GGTTTGTCCT ATAGACACCA TTCGTCAAGG ACGGGGCCGA GTCCCGGTTC
-------------------------------------------------------------------------------
5801  AACAGATGGT CCCCAGATGC GGTCCAGCCC TCAGCAGTTT CTAGAGAACC
      TTGTCTACCA GGGGTCTACG CCAGGTCGGG AGTCGTCAAA GATCTCTTGG
-------------------------------------------------------------------------------
5851  ATCAGATGTT TCCAGGGTGC CCCAAGGACC TGAAATGACC CTGTGCCTTA
      TAGTCTACAA AGGTCCCACG GGGTTCCTGG ACTTTACTGG GACACGGAAT
-------------------------------------------------------------------------------
5901  TTTGAACTAA CCAATCAGTT CGCTTCTCGC TTCTGTTCGC GCGCTTCTGC
      AAACTTGATT GGTTAGTCAA GCGAAGAGCG AAGACAAGCG CGCGAAGACG
-------------------------------------------------------------------------------
5951  TCCCCGAGCT CAATAAAAGA GCCCACAACC CCTCACTCGG GGCGCCAGTC
      AGGGGCTCGA GTTATTTTCT CGGGTGTTGG GGAGTGAGCC CCGCGGTCAG
-------------------------------------------------------------------------------
6001  CTCCGATTGA CTGAGTCGCC CGGGTACCCG TGTATCCAAT AAACCCTCTT
      GAGGCTAACT GACTCAGCGG GCCCATGGGC ACATAGGTTA TTTGGGAGAA
-------------------------------------------------------------------------------
6051  GCAGTTGCAT CCGACTTGTG GTCTCGCTGT TCCTTGGGAG GGTCTCCTCT
      CGTCAACGTA GGCTGAACAC CAGAGCGACA AGGAACCCTC CCAGAGGAGA
-------------------------------------------------------------------------------
6101  GAGTGATTGA CTACCCGTCA GCGGGGGTCT TTCATTCATG CAGCATGTAT
      CTCACTAACT GATGGGCAGT CGCCCCCAGA AAGTAAGTAC GTCGTACATA
-------------------------------------------------------------------------------
6151  CAAAATTAAT TTGGTTTTTT TTCTTAAGTA TTTACATTAA ATGGCCATAG
      GTTTTAATTA AACCAAAAAA AAGAATTCAT AAATGTAATT TACCGGTATC
-------------------------------------------------------------------------------
6201  TTGCATTAAT GAATCGGCCA ACGCGCGGGG AGAGGCGGTT TGCGTATTGG
      AACGTAATTA CTTAGCCGGT TGCGCGCCCC TCTCCGCCAA ACGCATAACC
-------------------------------------------------------------------------------
6251  CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG TCGTTCGGCT
      GCGAGAAGGC GAAGGAGCGA GTGACTGAGC GACGCGAGCC AGCAAGCCGA
-------------------------------------------------------------------------------
6301  GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
      CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC
-------------------------------------------------------------------------------
6351  AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG
      TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC
-------------------------------------------------------------------------------
6401  GCCAGGAACC GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG
      CGGTCCTTGG CATTTTTCCG GCGCAACGAC CGCAAAAAGG TATCCGAGGC
-------------------------------------------------------------------------------
6451  CCCCCCTGAC GAGCATCACA AAAATCGACG CTCAAGTCAG AGGTGGCGAA
      GGGGGGACTG CTCGTAGTGT TTTTAGCTGC GAGTTCAGTC TCCACCGCTT
-------------------------------------------------------------------------------
6501  ACCCGACAGG ACTATAAAGA TACCAGGCGT TTCCCCCTGG AAGCTCCCTC
      TGGGCTGTCC TGATATTTCT ATGGTCCGCA AAGGGGGACC TTCGAGGGAG
-------------------------------------------------------------------------------
6551  GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC TGTCCGCCTT
      CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG ACAGGCGGAA
-------------------------------------------------------------------------------
6601  TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA TAGCTCACGC TGTAGGTATC
      AGAGGGAAGC CCTTCGCACC GCGAAAGAGT ATCGAGTGCG ACATCCATAG
-------------------------------------------------------------------------------
```

```
6651  TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC
      AGTCAAGCCA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG
------------------------------------------------------------------------------
6701  CCCGTTCAGC CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC
      GGGCAAGTCG GGCTGGCGAC GCGGAATAGG CCATTGATAG CAGAACTCAG
------------------------------------------------------------------------------
6751  CAACCCGGTA AGACACGACT TATCGCCACT GGCAGCAGCC ACTGGTAACA
      GTTGGGCCAT TCTGTGCTGA ATAGCGGTGA CCGTCGTCGG TGACCATTGT
------------------------------------------------------------------------------
6801  GGATTAGCAG AGCGAGGTAT GTAGGCGGTG CTACAGAGTT CTTGAAGTGG
      CCTAATCGTC TCGCTCCATA CATCCGCCAC GATGTCTCAA GAACTTCACC
------------------------------------------------------------------------------
6851  TGGCCTAACT ACGGCTACAC TAGAAGAACA GTATTTGGTA TCTGCGCTCT
      ACCGGATTGA TGCCGATGTG ATCTTCTTGT CATAAACCAT AGACGCGAGA
------------------------------------------------------------------------------
6901  GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA
      CGACTTCGGT CAATGGAAGC CTTTTTCTCA ACCATCGAGA ACTAGGCCGT
------------------------------------------------------------------------------
6951  AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT
      TTGTTTGGTG GCGACCATCG CCACCAAAAA AACAAACGTT CGTCGTCTAA
------------------------------------------------------------------------------
7001  ACGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG
      TGCGCGTCTT TTTTTCCTAG AGTTCTTCTA GGAAACTAGA AAAGATGCCC
------------------------------------------------------------------------------
7051  GTCTGACGCT CAGTGGAACG AAAACTCACG TTAAGGGATT TTGGTCATGA
      CAGACTGCGA GTCACCTTGC TTTTGAGTGC AATTCCCTAA AACCAGTACT
------------------------------------------------------------------------------
7101  GATTATCAAA AAGGATCTTC ACCTAGATCC TTTTAAATTA AAAATGAAGT
      CTAATAGTTT TTCCTAGAAG TGGATCTAGG AAAATTTAAT TTTTACTTCA
------------------------------------------------------------------------------
7151  TTGCGGCCGC AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA
      AACGCCGGCG TTTAGTTAGA TTTCATATAT ACTCATTTGA ACCAGACTGT
------------------------------------------------------------------------------
7201  GTTACCAATG CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT
      CAATGGTTAC GAATTAGTCA CTCCGTGGAT AGAGTCGCTA GACAGATAAA
------------------------------------------------------------------------------
7251  CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTGTAGATAA CTACGATACG
      GCAAGTAGGT ATCAACGGAC TGAGGGGCAG CACATCTATT GATGCTATGC
------------------------------------------------------------------------------
7301  GGAGGGCTTA CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC
      CCTCCCGAAT GGTAGACCGG GGTCACGACG TTACTATGGC GCTCTGGGTG
------------------------------------------------------------------------------
7351  GCTCACCGGC TCCAGATTTA TCAGCAATAA ACCAGCCAGC CGGAAGGGCC
      CGAGTGGCCG AGGTCTAAAT AGTCGTTATT TGGTCGGTCG GCCTTCCCGG
------------------------------------------------------------------------------
7401  GAGCGCAGAA GTGGTCCTGC AACTTTATCC GCCTCCATCC AGTCTATTAA
      CTCGCGTCTT CACCAGGACG TTGAAATAGG CGGAGGTAGG TCAGATAATT
------------------------------------------------------------------------------
7451  TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCGCA
      AACAACGGCC CTTCGATCTC ATTCATCAAG CGGTCAATTA TCAAACGCGT
------------------------------------------------------------------------------
7501  ACGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTTGGT
      TGCAACAACG GTAACGATGT CCGTAGCACC ACAGTGCGAG CAGCAAACCA
------------------------------------------------------------------------------
7551  ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC
      TACCGAAGTA AGTCGAGGCC AAGGGTTGCT AGTTCCGCTC AATGTACTAG
------------------------------------------------------------------------------
```

```
7601  CCCCATGTTG TGCAAAAAAG CGGTTAGCTC CTTCGGTCCT CCGATCGTTG
      GGGGTACAAC ACGTTTTTTC GCCAATCGAG GAAGCCAGGA GGCTAGCAAC
-------------------------------------------------------------------------------
7651  TCAGAAGTAA GTTGGCCGCA GTGTTATCAC TCATGGTTAT GGCAGCACTG
      AGTCTTCATT CAACCGGCGT CACAATAGTG AGTACCAATA CCGTCGTGAC
-------------------------------------------------------------------------------
7701  CATAATTCTC TTACTGTCAT GCCATCCGTA AGATGCTTTT CTGTGACTGG
      GTATTAAGAG AATGACAGTA CGGTAGGCAT TCTACGAAAA GACACTGACC
-------------------------------------------------------------------------------
7751  TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT
      ACTCATGAGT TGGTTCAGTA AGACTCTTAT CACATACGCC GCTGGCTCAA
-------------------------------------------------------------------------------
7801  GCTCTTGCCC GGCGTCAATA CGGGATAATA CCGCGCCACA TAGCAGAACT
      CGAGAACGGG CCGCAGTTAT GCCCTATTAT GGCGCGGTGT ATCGTCTTGA
-------------------------------------------------------------------------------
7851  TTAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG
      AATTTTCACG AGTAGTAACC TTTTGCAAGA AGCCCCGCTT TTGAGAGTTC
-------------------------------------------------------------------------------
7901  GATCTTACCG CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA
      CTAGAATGGC GACAACTCTA GGTCAAGCTA CATTGGGTGA GCACGTGGGT
-------------------------------------------------------------------------------
7951  ACTGATCTTC AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA
      TGACTAGAAG TCGTAGAAAA TGAAAGTGGT CGCAAAGACC CACTCGTTTT
-------------------------------------------------------------------------------
8001  ACAGGAAGGC AAAATGCCGC AAAAAAGGGA ATAAGGGCGA CACGGAAATG
      TGTCCTTCCG TTTTACGGCG TTTTTTCCCT TATTCCCGCT GTGCCTTTAC
-------------------------------------------------------------------------------
8051  TTGAATACTC ATACTCTTCC TTTTTCAATA TTATTGAAGC ATTTATCAGG
      AACTTATGAG TATGAGAAGG AAAAAGTTAT AATAACTTCG TAAATAGTCC
-------------------------------------------------------------------------------
8101  GTTATTGTCT CATGAGCGGA TACATATTTG AATGTATTTA GAAAAATAAA
      CAATAACAGA GTACTCGCCT ATGTATAAAC TTACATAAAT CTTTTTATTT
-------------------------------------------------------------------------------
8151  CAAATAGGGG TTCCGCGCAC ATTTC
      GTTTATCCCC AAGGCGCGTG TAAAG
-------------------------------------------------------------------------------
```

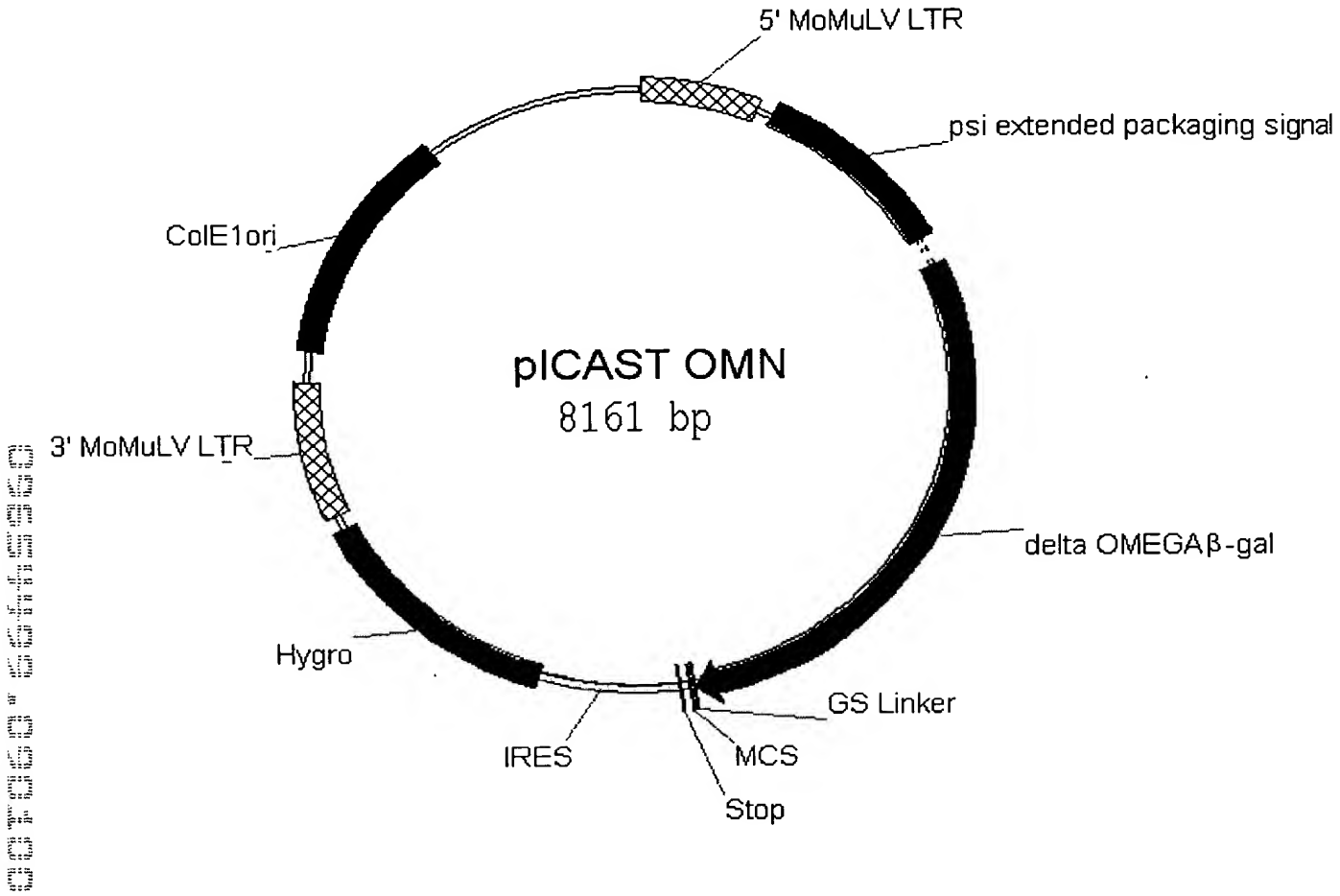
5' MoMuLV LTR
psi extended packaging signal
ColE1ori
pICAST OMN
8161 bp
3' MoMuLV LTR
delta OMEGAβ-gal
Hygro
GS Linker
IRES
MCS
Stop

Figure 13A

```
  1  CTGCAGCCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG
     GACGTCGGAC TTATACCCGG TTTGTCCTAT AGACACCATT CGTCAAGGAC
---------------------------------------------------------------------------
 51  CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA
     GGGGCCGAGT CCCGGTTCTT GTCTACCTTG TCGACTTATA CCCGGTTTGT
---------------------------------------------------------------------------
101  GGATATCTGT GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT
     CCTATAGACA CCATTCGTCA AGGACGGGGC CGAGTCCCGG TTCTTGTCTA
---------------------------------------------------------------------------
151  GGTCCCCAGA TGCGGTCCAG CCCTCAGCAG TTTCTAGAGA ACCATCAGAT
     CCAGGGGTCT ACGCCAGGTC GGGAGTCGTC AAAGATCTCT TGGTAGTCTA
---------------------------------------------------------------------------
201  GTTTCCAGGG TGCCCCAAGG ACCTGAAATG ACCCTGTGCC TTATTTGAAC
     CAAAGGTCCC ACGGGGTTCC TGGACTTTAC TGGGACACGG AATAAACTTG
---------------------------------------------------------------------------
251  TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC TGCTCCCCGA
     ATTGGTTAGT CAAGCGAAGA GCGAAGACAA GCGCGCGAAG ACGAGGGGCT
---------------------------------------------------------------------------
301  GCTCAATAAA AGAGCCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT
     CGAGTTATTT TCTCGGGTGT TGGGGAGTGA GCCCCGCGGT CAGGAGGCTA
---------------------------------------------------------------------------
351  TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCCT CTTGCAGTTG
     ACTGACTCAG CGGGCCCATG GGCACATAGG TTATTTGGGA GAACGTCAAC
---------------------------------------------------------------------------
401  CATCCGACTT GTGGTCTCGC TGTTCCTTGG GAGGGTCTCC TCTGAGTGAT
     GTAGGCTGAA CACCAGAGCG ACAAGGAACC CTCCCAGAGG AGACTCACTA
---------------------------------------------------------------------------
451  TGACTACCCG TCAGCGGGGG TCTTTCATTT GGGGGCTCGT CCGGGATCGG
     ACTGATGGGC AGTCGCCCCC AGAAAGTAAA CCCCCGAGCA GGCCCTAGCC
---------------------------------------------------------------------------
501  GAGACCCCTG CCCAGGGACC ACCGACCCAC CACCGGGAGG CAAGCTGGCC
     CTCTGGGGAC GGGTCCCTGG TGGCTGGGTG GTGGCCCTCC GTTCGACCGG
---------------------------------------------------------------------------
551  AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG ACTGATTTTA
     TCGTTGAATA GACACAGACA GGCTAACAGA TCACAGATAC TGACTAAAAT
---------------------------------------------------------------------------
601  TGCGCCTGCG TCGGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC
     ACGCGGACGC AGCCATGATC AATCGATTGA TCGAGACATA GACCGCCTGG
---------------------------------------------------------------------------
651  CGTGGTGGAA CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG
     GCACCACCTT GACTGCTCAA GACTTGTGGG CCGGCGTTGG GACCCTCTGC
---------------------------------------------------------------------------
701  TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG CCCGACCTGA GGAAGGGAGT
     AGGGTCCCTG AAACCCCCGG CAAAAACACC GGGCTGGACT CCTTCCCTCA
---------------------------------------------------------------------------
751  CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCTGGT AGGAGACGAG
     GCTACACCTT AGGCTGGGGC AGTCCTATAC ACCAAGACCA TCCTCTGCTC
---------------------------------------------------------------------------
801  AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA
     TTGGATTTTG TCAAGGGCGG AGGCAGACTT AAAAACGAAA GCCAAACCTT
---------------------------------------------------------------------------
851  CCGAAGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT
     GGCTTCGGCG CGCAGAACAG ACGACGTCGT AGCAAGACAC AACAGAGACA
---------------------------------------------------------------------------
901  CTGACTGTGT TTCTGTATTT GTCTGAAAAT TAGGGCCAGA CTGTTACCAC
     GACTGACACA AAGACATAAA CAGACTTTTA ATCCCGGTCT GACAATGGTG
---------------------------------------------------------------------------
```

FIGURE 13B

```
 951  TCCCTTAAGT TTGACCTTAG GTAACTGGAA AGATGTCGAG CGGCTCGCTC
      AGGGAATTCA AACTGGAATC CATTGACCTT TCTACAGCTC GCCGAGCGAG
-------------------------------------------------------------------------------
1001  ACAACCAGTC GGTAGATGTC AAGAAGAGAC GTTGGGTTAC CTTCTGCTCT
      TGTTGGTCAG CCATCTACAG TTCTTCTCTG CAACCCAATG GAAGACGAGA
-------------------------------------------------------------------------------
1051  GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG GCACCTTTAA
      CGTCTTACCG GTTGGAAATT GCAGCCTACC GGCGCTCTGC CGTGGAAATT
-------------------------------------------------------------------------------
1101  CCGAGACCTC ATCACCCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC
      GGCTCTGGAG TAGTGGGTCC AATTCTAGTT CCAGAAAAGT GGACCGGGCG
-------------------------------------------------------------------------------
1151  ATGGACACCC AGACCAGGTC CCCTACATCG TGACCTGGGA AGCCTTGGCT
      TACCTGTGGG TCTGGTCCAG GGGATGTAGC ACTGGACCCT TCGGAACCGA
-------------------------------------------------------------------------------
1201  TTTGACCCCC CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC
      AAACTGGGGG GAGGGACCCA GTTCGGGAAA CATGTGGGAT TCGGAGGCGG
-------------------------------------------------------------------------------
1251  TCCTCTTCCT CCATCCGCCC CGTCTCTCCC CCTTGAACCT CCTCGTTCGA
      AGGAGAAGGA GGTAGGCGGG GCAGAGAGGG GGAACTTGGA GGAGCAAGCT
-------------------------------------------------------------------------------
1301  CCCCGCCTCG ATCCTCCCTT TATCCAGCCC TCACTCCTTC TCTAGGCGCC
      GGGGCGGAGC TAGGAGGGAA ATAGGTCGGG AGTGAGGAAG AGATCCGCGG
-------------------------------------------------------------------------------
1351  GGCCGCTCTA GCCCATTAAT ACGACTCACT ATAGGGCGAT TCGAACACCA
      CCGGCGAGAT CGGGTAATTA TGCTGAGTGA TATCCCGCTA AGCTTGTGGT
-------------------------------------------------------------------------------
1401  TGCACCATCA TCATCATCAC GTCGACGAAC AGAAACTCAT TTCCGAAGAA
      ACGTGGTAGT AGTAGTAGTG CAGCTGCTTG TCTTTGAGTA AAGGCTTCTT
-------------------------------------------------------------------------------
1451  GACCTACTCG AGATGGGCGT GATTACGGAT TCACTGGCCG TCGTTTTACA
      CTGGATGAGC TCTACCCGCA CTAATGCCTA AGTGACCGGC AGCAAAATGT
-------------------------------------------------------------------------------
1501  ACGTCGTGAC TGGGAAAACC CTGGCGTTAC CCAACTTAAT CGCCTTGCAG
      TGCAGCACTG ACCCTTTTGG GACCGCAATG GGTTGAATTA GCGGAACGTC
-------------------------------------------------------------------------------
1551  CACATCCCCC TTTCGCCAGC TGGCGTAATA GCGAAGAGGC CCGCACCGAT
      GTGTAGGGGG AAAGCGGTCG ACCGCATTAT CGCTTCTCCG GGCGTGGCTA
-------------------------------------------------------------------------------
1601  CGCCCTTCCC AACAGTTACG CAGCCTGAAT GGCGAATGGC GCTTTGCCTG
      GCGGGAAGGG TTGTCAATGC GTCGGACTTA CCGCTTACCG CGAAACGGAC
-------------------------------------------------------------------------------
1651  GTTTCCGGCA CCAGAAGCGG TGCCGGAAAG CTGGCTGGAG TGCGATCTTC
      CAAAGGCCGT GGTCTTCGCC ACGGCCTTTC GACCGACCTC ACGCTAGAAG
-------------------------------------------------------------------------------
1701  CTGAGGCCGA TACTGTCGTC GTCCCCTCAA ACTGGCAGAT GCACGGTTAC
      GACTCCGGCT ATGACAGCAG CAGGGGAGTT TGACCGTCTA CGTGCCAATG
-------------------------------------------------------------------------------
1751  GATGCGCCCA TCTACACCAA CGTGACCTAT CCCATTACGG TCAATCCGCC
      CTACGCGGGT AGATGTGGTT GCACTGGATA GGGTAATGCC AGTTAGGCGG
-------------------------------------------------------------------------------
1801  GTTTGTTCCC ACGGAGAATC CGACGGGTTG TTACTCGCTC ACATTTAATG
      CAAACAAGGG TGCCTCTTAG GCTGCCCAAC AATGAGCGAG TGTAAATTAC
-------------------------------------------------------------------------------
1851  TTGATGAAAG CTGGCTACAG GAAGGCCAGA CGCGAATTAT TTTTGATGGC
      AACTACTTTC GACCGATGTC CTTCCGGTCT GCGCTTAATA AAAACTACCG
-------------------------------------------------------------------------------
```

```
1901  GTTAACTCGG CGTTTCATCT GTGGTGCAAC GGGCGCTGGG TCGGTTACGG
      CAATTGAGCC GCAAAGTAGA CACCACGTTG CCCGCGACCC AGCCAATGCC
 ----------------------------------------------------------------------------
1951  CCAGGACAGT CGTTTGCCGT CTGAATTTGA CCTGAGCGCA TTTTTACGCG
      GGTCCTGTCA GCAAACGGCA GACTTAAACT GGACTCGCGT AAAAATGCGC
 ----------------------------------------------------------------------------
2001  CCGGAGAAAA CCGCCTCGCG GTGATGGTGC TGCGCTGGAG TGACGGCAGT
      GGCCTCTTTT GGCGGAGCGC CACTACCACG ACGCGACCTC ACTGCCGTCA
 ----------------------------------------------------------------------------
2051  TATCTGGAAG ATCAGGATAT GTGGCGGATG AGCGGCATTT TCCGTGACGT
      ATAGACCTTC TAGTCCTATA CACCGCCTAC TCGCCGTAAA AGGCACTGCA
 ----------------------------------------------------------------------------
2101  CTCGTTGCTG CATAAACCGA CTACACAAAT CAGCGATTTC CATGTTGCCA
      GAGCAACGAC GTATTTGGCT GATGTGTTTA GTCGCTAAAG GTACAACGGT
 ----------------------------------------------------------------------------
2151  CTCGCTTTAA TGATGATTTC AGCCGCGCTG TACTGGAGGC TGAAGTTCAG
      GAGCGAAATT ACTACTAAAG TCGGCGCGAC ATGACCTCCG ACTTCAAGTC
 ----------------------------------------------------------------------------
2201  ATGTGCGGCG AGTTGCGTGA CTACCTACGG GTAACAGTTT CTTTATGGCA
      TACACGCCGC TCAACGCACT GATGGATGCC CATTGTCAAA GAAATACCGT
 ----------------------------------------------------------------------------
2251  GGGTGAAACG CAGGTCGCCA GCGGCACCGC GCCTTTCGGC GGTGAAATTA
      CCCACTTTGC GTCCAGCGGT CGCCGTGGCG CGGAAAGCCG CCACTTTAAT
 ----------------------------------------------------------------------------
2301  TCGATGAGCG TGGTGGTTAT GCCGATCGCG TCACACTACG TCTGAACGTC
      AGCTACTCGC ACCACCAATA CGGCTAGCGC AGTGTGATGC AGACTTGCAG
 ----------------------------------------------------------------------------
2351  GAAAACCCGA AACTGTGGAG CGCCGAAATC CCGAATCTCT ATCGTGCGGT
      CTTTTGGGCT TTGACACCTC GCGGCTTTAG GGCTTAGAGA TAGCACGCCA
 ----------------------------------------------------------------------------
2401  GGTTGAACTG CACACCGCCG ACGGCACGCT GATTGAAGCA GAAGCCTGCG
      CCAACTTGAC GTGTGGCGGC TGCCGTGCGA CTAACTTCGT CTTCGGACGC
 ----------------------------------------------------------------------------
2451  ATGTCGGTTT CCGCGAGGTG CGGATTGAAA ATGGTCTGCT GCTGCTGAAC
      TACAGCCAAA GGCGCTCCAC GCCTAACTTT TACCAGACGA CGACGACTTG
 ----------------------------------------------------------------------------
2501  GGCAAGCCGT TGCTGATTCG AGGCGTTAAC CGTCACGAGC ATCATCCTCT
      CCGTTCGGCA ACGACTAAGC TCCGCAATTG GCAGTGCTCG TAGTAGGAGA
 ----------------------------------------------------------------------------
2551  GCATGGTCAG GTCATGGATG AGCAGACGAT GGTGCAGGAT ATCCTGCTGA
      CGTACCAGTC CAGTACCTAC TCGTCTGCTA CCACGTCCTA TAGGACGACT
 ----------------------------------------------------------------------------
2601  TGAAGCAGAA CAACTTTAAC GCCGTGCGCT GTTCGCATTA TCCGAACCAT
      ACTTCGTCTT GTTGAAATTG CGGCACGCGA CAAGCGTAAT AGGCTTGGTA
 ----------------------------------------------------------------------------
2651  CCGCTGTGGT ACACGCTGTG CGACCGCTAC GGCCTGTATG TGGTGGATGA
      GGCGACACCA TGTGCGACAC GCTGGCGATG CCGGACATAC ACCACCTACT
 ----------------------------------------------------------------------------
2701  AGCCAATATT GAAACCCACG GCATGGTGCC AATGAATCGT CTGACCGATG
      TCGGTTATAA CTTTGGGTGC CGTACCACGG TTACTTAGCA GACTGGCTAC
 ----------------------------------------------------------------------------
2751  ATCCGCGCTG GCTACCGGCG ATGAGCGAAC GCGTAACGCG AATGGTGCAG
      TAGGCGCGAC CGATGGCCGC TACTCGCTTG CGCATTGCGC TTACCACGTC
 ----------------------------------------------------------------------------
2801  CGCGATCGTA ATCACCCGAG TGTGATCATC TGGTCGCTGG GGAATGAATC
      GCGCTAGCAT TAGTGGGCTC ACACTAGTAG ACCAGCGACC CCTTACTTAG
 ----------------------------------------------------------------------------
```

```
2851  AGGCCACGGC GCTAATCACG ACGCGCTGTA TCGCTGGATC AAATCTGTCG
      TCCGGTGCCG CGATTAGTGC TGCGCGACAT AGCGACCTAG TTTAGACAGC
-------------------------------------------------------------------------------
2901  ATCCTTCCCG CCCGGTGCAG TATGAAGGCG GCGGAGCCGA CACCACGGCC
      TAGGAAGGGC GGGCCACGTC ATACTTCCGC CGCCTCGGCT GTGGTGCCGG
-------------------------------------------------------------------------------
2951  ACCGATATTA TTTGCCCGAT GTACGCGCGC GTGGATGAAG ACCAGCCCTT
      TGGCTATAAT AAACGGGCTA CATGCGCGCG CACCTACTTC TGGTCGGGAA
-------------------------------------------------------------------------------
3001  CCCGGCTGTG CCGAAATGGT CCATCAAAAA ATGGCTTTCG CTACCTGGAG
      GGGCCGACAC GGCTTTACCA GGTAGTTTTT TACCGAAAGC GATGGACCTC
-------------------------------------------------------------------------------
3051  AGACGCGCCC GCTGATCCTT TGCGAATACG CCCACGCGAT GGGTAACAGT
      TCTGCGCGGG CGACTAGGAA ACGCTTATGC GGGTGCGCTA CCCATTGTCA
-------------------------------------------------------------------------------
3101  CTTGGCGGTT TCGCTAAATA CTGGCAGGCG TTTCGTCAGT ATCCCCGTTT
      GAACCGCCAA AGCGATTTAT GACCGTCCGC AAAGCAGTCA TAGGGGCAAA
-------------------------------------------------------------------------------
3151  ACAGGGCGGC TTCGTCTGGG ACTGGGTGGA TCAGTCGCTG ATTAAATATG
      TGTCCCGCCG AAGCAGACCC TGACCCACCT AGTCAGCGAC TAATTTATAC
-------------------------------------------------------------------------------
3201  ATGAAAACGG CAACCCGTGG TCGGCTTACG GCGGTGATTT TGGCGATACG
      TACTTTTGCC GTTGGGCACC AGCCGAATGC CGCCACTAAA ACCGCTATGC
-------------------------------------------------------------------------------
3251  CCGAACGATC GCCAGTTCTG TATGAACGGT CTGGTCTTTG CCGACCGCAC
      GGCTTGCTAG CGGTCAAGAC ATACTTGCCA GACCAGAAAC GGCTGGCGTG
-------------------------------------------------------------------------------
3301  GCCGCATCCA GCGCTGACGG AAGCAAAACA CCAGCAGCAG TTTTTCCAGT
      CGGCGTAGGT CGCGACTGCC TTCGTTTTGT GGTCGTCGTC AAAAAGGTCA
-------------------------------------------------------------------------------
3351  TCCGTTTATC CGGGCAAACC ATCGAAGTGA CCAGCGAATA CCTGTTCCGT
      AGGCAAATAG GCCCGTTTGG TAGCTTCACT GGTCGCTTAT GGACAAGGCA
-------------------------------------------------------------------------------
3401  CATAGCGATA ACGAGCTCCT GCACTGGATG GTGGCGCTGG ATGGTAAGCC
      GTATCGCTAT TGCTCGAGGA CGTGACCTAC CACCGCGACC TACCATTCGG
-------------------------------------------------------------------------------
3451  GCTGGCAAGC GGTGAAGTGC CTCTGGATGT CGCTCCACAA GGTAAACAGT
      CGACCGTTCG CCACTTCACG GAGACCTACA GCGAGGTGTT CCATTTGTCA
-------------------------------------------------------------------------------
3501  TGATTGAACT GCCTGAACTA CCGCAGCCGG AGAGCGCCGG GCAACTCTGG
      ACTAACTTGA CGGACTTGAT GGCGTCGGCC TCTCGCGGCC CGTTGAGACC
-------------------------------------------------------------------------------
3551  CTCACAGTAC GCGTAGTGCA ACCGAACGCG ACCGCATGGT CAGAAGCCGG
      GAGTGTCATG CGCATCACGT TGGCTTGCGC TGGCGTACCA GTCTTCGGCC
-------------------------------------------------------------------------------
3601  GCACATCAGC GCCTGGCAGC AGTGGCGTCT GGCGGAAAAC CTCAGTGTGA
      CGTGTAGTCG CGGACCGTCG TCACCGCAGA CCGCCTTTTG GAGTCACACT
-------------------------------------------------------------------------------
3651  CGCTCCCCGC CGCGTCCCAC GCCATCCCGC ATCTGACCAC CAGCGAAATG
      GCGAGGGGCG GCGCAGGGTG CGGTAGGGCG TAGACTGGTG GTCGCTTTAC
-------------------------------------------------------------------------------
3701  GATTTTTGCA TCGAGCTGGG TAATAAGCGT TGGCAATTTA ACCGCCAGTC
      CTAAAAACGT AGCTCGACCC ATTATTCGCA ACCGTTAAAT TGGCGGTCAG
-------------------------------------------------------------------------------
3751  AGGCTTTCTT TCACAGATGT GGATTGGCGA TAAAAAACAA CTGCTGACGC
      TCCGAAAGAA AGTGTCTACA CCTAACCGCT ATTTTTTGTT GACGACTGCG
-------------------------------------------------------------------------------
```

```
3801  CGCTGCGCGA TCAGTTCACC CGTGTCGATA GATCTGGAGG TGGTGGCAGC
      GCGACGCGCT AGTCAAGTGG GCACAGCTAT CTAGACCTCC ACCACCGTCG

3851  AGGCCTTGGC GCGCCGGATC CTTAATTAAC AATTGACCGG TAATAATAGG
      TCCGGAACCG CGCGGCCTAG GAATTAATTG TTAACTGGCC ATTATTATCC

3901  TAGATAAGTG ACTGATTAGA TGCATTTCGA CTAGATCCCT CGACCAATTC
      ATCTATTCAC TGACTAATCT ACGTAAAGCT GATCTAGGGA GCTGGTTAAG

3951  CGGTTATTTT CCACCATATT GCCGTCTTTT GGCAATGTGA GGGCCCGGAA
      GCCAATAAAA GGTGGTATAA CGGCAGAAAA CCGTTACACT CCCGGGCCTT

4001  ACCTGGCCCT GTCTTCTTGA CGAGCATTCC TAGGGGTCTT TCCCCTCTCG
      TGGACCGGGA CAGAAGAACT GCTCGTAAGG ATCCCCAGAA AGGGGAGAGC

4051  CCAAAGGAAT GCAAGGTCTG TTGAATGTCG TGAAGGAAGC AGTTCCTCTG
      GGTTTCCTTA CGTTCCAGAC AACTTACAGC ACTTCCTTCG TCAAGGAGAC

4101  GAAGCTTCTT GAAGACAAAC AACGTCTGTA GCGACCCTTT GCAGGCAGCG
      CTTCGAAGAA CTTCTGTTTG TTGCAGACAT CGCTGGGAAA CGTCCGTCGC

4151  GAACCCCCCA CCTGGCGACA GGTGCCTCTG CGGCCAAAAG CCACGTGTAT
      CTTGGGGGGT GGACCGCTGT CCACGGAGAC GCCGGTTTTC GGTGCACATA

4201  AAGATACACC TGCAAAGGCG GCACAACCCC AGTGCCACGT TGTGAGTTGG
      TTCTATGTGG ACGTTTCCGC CGTGTTGGGG TCACGGTGCA ACACTCAACC

4251  ATAGTTGTGG AAAGAGTCAA ATGGCTCTCC TCAAGCGTAT TCAACAAGGG
      TATCAACACC TTTCTCAGTT TACCGAGAGG AGTTCGCATA AGTTGTTCCC

4301  GCTGAAGGAT GCCCAGAAGG TACCCCATTG TATGGGATCT GATCTGGGGC
      CGACTTCCTA CGGGTCTTCC ATGGGGTAAC ATACCCTAGA CTAGACCCCG

4351  CTCGGTGCAC ATGCTTTACA TGTGTTTAGT CGAGGTTAAA AAACGTCTAG
      GAGCCACGTG TACGAAATGT ACACAAATCA GCTCCAATTT TTTGCAGATC

4401  GCCCCCCGAA CCACGGGGAC GTGGTTTTCC TTTGAAAAAC ACGATGATAA
      CGGGGGGCTT GGTGCCCCTG CACCAAAAGG AAACTTTTTG TGCTACTATT

4451  TACCATGAAA AAGCCTGAAC TCACCGCGAC GTCTGTCGAG AAGTTTCTGA
      ATGGTACTTT TTCGGACTTG AGTGGCGCTG CAGACAGCTC TTCAAAGACT

4501  TCGAAAAGTT CGACAGCGTC TCCGACCTGA TGCAGCTCTC GGAGGGCGAA
      AGCTTTTCAA GCTGTCGCAG AGGCTGGACT ACGTCGAGAG CCTCCCGCTT

4551  GAATCTCGTG CTTTCAGCTT CGATGTAGGA GGGCGTGGAT ATGTCCTGCG
      CTTAGAGCAC GAAAGTCGAA GCTACATCCT CCCGCACCTA TACAGGACGC

4601  GGTAAATAGC TGCGCCGATG GTTTCTACAA AGATCGTTAT GTTTATCGGC
      CCATTTATCG ACGCGGCTAC CAAAGATGTT TCTAGCAATA CAAATAGCCG

4651  ACTTTGCATC GGCCGCGCTC CCGATTCCGG AAGTGCTTGA CATTGGGGAA
      TGAAACGTAG CCGGCGCGAG GGCTAAGGCC TTCACGAACT GTAACCCCTT

4701  TTTAGCGAGA GCCTGACCTA TTGCATCTCC CGCCGTGCAC AGGGTGTCAC
      AAATCGCTCT CGGACTGGAT AACGTAGAGG GCGGCACGTG TCCCACAGTG
```

```
4751  GTTGCAAGAC CTGCCTGAAA CCGAACTGCC CGCTGTTCTG CAGCCGGTCG
      CAACGTTCTG GACGGACTTT GGCTTGACGG GCGACAAGAC GTCGGCCAGC
-------------------------------------------------------------------------------
4801  CGGAGGCCAT GGATGCGATC GCTGCGGCCG ATCTTAGCCA GACGAGCGGG
      GCCTCCGGTA CCTACGCTAG CGACGCCGGC TAGAATCGGT CTGCTCGCCC
-------------------------------------------------------------------------------
4851  TTCGGCCCAT TCGGACCGCA AGGAATCGGT CAATACACTA CATGGCGTGA
      AAGCCGGGTA AGCCTGGCGT TCCTTAGCCA GTTATGTGAT GTACCGCACT
-------------------------------------------------------------------------------
4901  TTTCATATGC GCGATTGCTG ATCCCCATGT GTATCACTGG CAAACTGTGA
      AAAGTATACG CGCTAACGAC TAGGGGTACA CATAGTGACC GTTTGACACT
-------------------------------------------------------------------------------
4951  TGGACGACAC CGTCAGTGCG TCCGTCGCGC AGGCTCTCGA TGAGCTGATG
      ACCTGCTGTG GCAGTCACGC AGGCAGCGCG TCCGAGAGCT ACTCGACTAC
-------------------------------------------------------------------------------
5001  CTTTGGGCCG AGGACTGCCC CGAAGTCCGG CACCTCGTGC ACGCGGATTT
      GAAACCCGGC TCCTGACGGG GCTTCAGGCC GTGGAGCACG TGCGCCTAAA
-------------------------------------------------------------------------------
5051  CGGCTCCAAC AATGTCCTGA CGGACAATGG CCGCATAACA GCGGTCATTG
      GCCGAGGTTG TTACAGGACT GCCTGTTACC GGCGTATTGT CGCCAGTAAC
-------------------------------------------------------------------------------
5101  ACTGGAGCGA GGCGATGTTC GGGGATTCCC AATACGAGGT CGCCAACATC
      TGACCTCGCT CCGCTACAAG CCCCTAAGGG TTATGCTCCA GCGGTTGTAG
-------------------------------------------------------------------------------
5151  TTCTTCTGGA GGCCGTGGTT GGCTTGTATG GAGCAGCAGA CGCGCTACTT
      AAGAAGACCT CCGGCACCAA CCGAACATAC CTCGTCGTCT GCGCGATGAA
-------------------------------------------------------------------------------
5201  CGAGCGGAGG CATCCGGAGC TTGCAGGATC GCCGCGGCTC CGGGCGTATA
      GCTCGCCTCC GTAGGCCTCG AACGTCCTAG CGGCGCCGAG GCCCGCATAT
-------------------------------------------------------------------------------
5251  TGCTCCGCAT TGGTCTTGAC CAACTCTATC AGAGCTTGGT TGACGGCAAT
      ACGAGGCGTA ACCAGAACTG GTTGAGATAG TCTCGAACCA ACTGCCGTTA
-------------------------------------------------------------------------------
5301  TTCGATGATG CAGCTTGGGC GCAGGGTCGA TGCGACGCAA TCGTCCGATC
      AAGCTACTAC GTCGAACCCG CGTCCCAGCT ACGCTGCGTT AGCAGGCTAG
-------------------------------------------------------------------------------
5351  CGGAGCCGGG ACTGTCGGGC GTACACAAAT CGCCCGCAGA AGCGCGGCCG
      GCCTCGGCCC TGACAGCCCG CATGTGTTTA GCGGGCGTCT TCGCGCCGGC
-------------------------------------------------------------------------------
5401  TCTGGACCGA TGGCTGTGTA GAAGTACTCG CCGATAGTGG AAACCGACGC
      AGACCTGGCT ACCGACACAT CTTCATGAGC GGCTATCACC TTTGGCTGCG
-------------------------------------------------------------------------------
5451  CCCAGCACTC GTCCGAGGGC AAAGGAATAG AGTAGATGCC GACCGGGATC
      GGGTCGTGAG CAGGCTCCCG TTTCCTTATC TCATCTACGG CTGGCCCTAG
-------------------------------------------------------------------------------
5501  TATCGATAAA ATAAAAGATT TTATTTAGTC TCCAGAAAAA GGGGGGAATG
      ATAGCTATTT TATTTTCTAA AATAAATCAG AGGTCTTTTT CCCCCCTTAC
-------------------------------------------------------------------------------
5551  AAAGACCCCA CCTGTAGGTT TGGCAAGCTA GCTTAAGTAA CGCCATTTTG
      TTTCTGGGGT GGACATCCAA ACCGTTCGAT CGAATTCATT GCGGTAAAAC
-------------------------------------------------------------------------------
5601  CAAGGCATGG AAAAATACAT AACTGAGAAT AGAGAAGTTC AGATCAAGGT
      GTTCCGTACC TTTTTATGTA TTGACTCTTA TCTCTTCAAG TCTAGTTCCA
-------------------------------------------------------------------------------
5651  CAGGAACAGA TGGAACAGCT GAATATGGGC CAAACAGGAT ATCTGTGGTA
      GTCCTTGTCT ACCTTGTCGA CTTATACCCG GTTTGTCCTA TAGACACCAT
-------------------------------------------------------------------------------
```

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5701  AGCAGTTCCT GCCCCGGCTC AGGGCCAAGA ACAGATGGAA CAGCTGAATA
      TCGTCAAGGA CGGGGCCGAG TCCCGGTTCT TGTCTACCTT GTCGACTTAT
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      ACCCGGTTTG TCCTATAGAC ACCATTCGTC AAGGACGGGG CCGAGTCCCG
-------------------------------------------------------------------------------
5801  CAAGAACAGA TGGTCCCCAG ATGCGGTCCA GCCCTCAGCA GTTTCTAGAG
      GTTCTTGTCT ACCAGGGGTC TACGCCAGGT CGGGAGTCGT CAAAGATCTC
-------------------------------------------------------------------------------
5851  AACCATCAGA TGTTTCCAGG GTGCCCCAAG GACCTGAAAT GACCCTGTGC
      TTGGTAGTCT ACAAAGGTCC CACGGGGTTC CTGGACTTTA CTGGGACACG
-------------------------------------------------------------------------------
5901  CTTATTTGAA CTAACCAATC AGTTCGCTTC TCGCTTCTGT TCGCGCGCTT
      GAATAAACTT GATTGGTTAG TCAAGCGAAG AGCGAAGACA AGCGCGCGAA
-------------------------------------------------------------------------------
5951  CTGCTCCCCG AGCTCAATAA AAGAGCCCAC AACCCCTCAC TCGGGGCGCC
      GACGAGGGGC TCGAGTTATT TTCTCGGGTG TTGGGGAGTG AGCCCCGCGG
-------------------------------------------------------------------------------
6001  AGTCCTCCGA TTGACTGAGT CGCCCGGGTA CCCGTGTATC CAATAAACCC
      TCAGGAGGCT AACTGACTCA GCGGGCCCAT GGGCACATAG GTTATTTGGG
-------------------------------------------------------------------------------
6051  TCTTGCAGTT GCATCCGACT TGTGGTCTCG CTGTTCCTTG GGAGGGTCTC
      AGAACGTCAA CGTAGGCTGA ACACCAGAGC GACAAGGAAC CCTCCCAGAG
-------------------------------------------------------------------------------
6101  CTCTGAGTGA TTGACTACCC GTCAGCGGGG GTCTTTCATT CATGCAGCAT
      GAGACTCACT AACTGATGGG CAGTCGCCCC CAGAAAGTAA GTACGTCGTA
-------------------------------------------------------------------------------
6151  GTATCAAAAT TAATTTGGTT TTTTTTCTTA AGTATTTACA TTAAATGGCC
      CATAGTTTTA ATTAAACCAA AAAAAAGAAT TCATAAATGT AATTTACCGG
-------------------------------------------------------------------------------
6201  ATAGTTGCAT TAATGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA
      TATCAACGTA ATTACTTAGC CGGTTGCGCG CCCCTCTCCG CCAAACGCAT
-------------------------------------------------------------------------------
6251  TTGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC
      AACCGCGAGA AGGCGAAGGA GCGAGTGACT GAGCGACGCG AGCCAGCAAG
-------------------------------------------------------------------------------
6301  GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC
      CCGACGCCGC TCGCCATAGT CGAGTGAGTT TCCGCCATTA TGCCAATAGG
-------------------------------------------------------------------------------
6351  ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA
      TGTCTTAGTC CCCTATTGCG TCCTTTCTTG TACACTCGTT TTCCGGTCGT
-------------------------------------------------------------------------------
6401  AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC
      TTTCCGGTCC TTGGCATTTT TCCGGCGCAA CGACCGCAAA AAGGTATCCG
-------------------------------------------------------------------------------
6451  TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG
      AGGCGGGGGG ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC AGTCTCCACC
-------------------------------------------------------------------------------
6501  CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC
      GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGCAAAGGGG GACCTTCGAG
-------------------------------------------------------------------------------
6551  CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG
      GGAGCACGCG AGAGGACAAG GCTGGGACGG CGAATGGCCT ATGGACAGGC
-------------------------------------------------------------------------------
6601  CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG
      GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG TGCGACATCC
-------------------------------------------------------------------------------
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6651  TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA
      ATAGAGTCAA GCCACATCCA GCAAGCGAGG TTCGACCCGA CACACGTGCT
 ----------------------------------------------------------------------------

6701  ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG
      TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG ATAGCAGAAC
 ----------------------------------------------------------------------------

6751  AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT
      TCAGGTTGGG CCATTCTGTG CTGAATAGCG GTGACCGTCG TCGGTGACCA
 ----------------------------------------------------------------------------

6801  AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA
      TTGTCCTAAT CGTCTCGCTC CATACATCCG CCACGATGTC TCAAGAACTT
 ----------------------------------------------------------------------------

6851  GTGGTGGCCT AACTACGGCT ACACTAGAAG AACAGTATTT GGTATCTGCG
      CACCACCGGA TTGATGCCGA TGTGATCTTC TTGTCATAAA CCATAGACGC
 ----------------------------------------------------------------------------

6901  CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC
      GAGACGACTT CGGTCAATGG AAGCCTTTTT CTCAACCATC GAGAACTAGG
 ----------------------------------------------------------------------------

6951  GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA
      CCGTTTGTTT GGTGGCGACC ATCGCCACCA AAAAAACAAA CGTTCGTCGT
 ----------------------------------------------------------------------------

7001  GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA
      CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC TAGAAAAGAT
 ----------------------------------------------------------------------------

7051  CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC
      GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTCC CTAAAACCAG
 ----------------------------------------------------------------------------

7101  ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTGC GGCCGCAAAT
      TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAACG CCGGCGTTTA
 ----------------------------------------------------------------------------

7151  CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA CCAATGCTTA
      GTTAGATTTC ATATATACTC ATTTGAACCA GACTGTCAAT GGTTACGAAT
 ----------------------------------------------------------------------------

7201  ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT CATCCATAGT
      TAGTCACTCC GTGGATAGAG TCGCTAGACA GATAAAGCAA GTAGGTATCA
 ----------------------------------------------------------------------------

7251  TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG GGCTTACCAT
      ACGGACTGAG GGGCAGCACA TCTATTGATG CTATGCCCTC CCGAATGGTA
 ----------------------------------------------------------------------------

7301  CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC ACCGGCTCCA
      GACCGGGGTC ACGACGTTAC TATGGCGCTC TGGGTGCGAG TGGCCGAGGT
 ----------------------------------------------------------------------------

7351  GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC GCAGAAGTGG
      CTAAATAGTC GTTATTTGGT CGGTCGGCCT TCCCGGCTCG CGTCTTCACC
 ----------------------------------------------------------------------------

7401  TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT TGCCGGGAAG
      AGGACGTTGA AATAGGCGGA GGTAGGTCAG ATAATTAACA ACGGCCCTTC
 ----------------------------------------------------------------------------

7451  CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT TGTTGCCATT
      GATCTCATTC ATCAAGCGGT CAATTATCAA ACGCGTTGCA ACAACGGTAA
 ----------------------------------------------------------------------------

7501  GCTACAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG CTTCATTCAG
      CGATGTCCGT AGCACCACAG TGCGAGCAGC AAACCATACC GAAGTAAGTC
 ----------------------------------------------------------------------------

7551  CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC ATGTTGTGCA
      GAGGCCAAGG GTTGCTAGTT CCGCTCAATG TACTAGGGGG TACAACACGT
 ----------------------------------------------------------------------------
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7601  AAAAAGCGGT TAGCTCCTTC GGTCCTCCGA TCGTTGTCAG AAGTAAGTTG
      TTTTTCGCCA ATCGAGGAAG CCAGGAGGCT AGCAACAGTC TTCATTCAAC
-------------------------------------------------------------------------------
7651  GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA ATTCTCTTAC
      CGGCGTCACA ATAGTGAGTA CCAATACCGT CGTGACGTAT TAAGAGAATG
-------------------------------------------------------------------------------
7701  TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG TACTCAACCA
      ACAGTACGGT AGGCATTCTA CGAAAAGACA CTGACCACTC ATGAGTTGGT
-------------------------------------------------------------------------------
7751  AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC TTGCCCGGCG
      TCAGTAAGAC TCTTATCACA TACGCCGCTG GCTCAACGAG AACGGGCCGC
-------------------------------------------------------------------------------
7801  TCAATACGGG ATAATACCGC GCCACATAGC AGAACTTTAA AAGTGCTCAT
      AGTTATGCCC TATTATGGCG CGGTGTATCG TCTTGAAATT TTCACGAGTA
-------------------------------------------------------------------------------
7851  CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC TTACCGCTGT
      GTAACCTTTT GCAAGAAGCC CCGCTTTTGA GAGTTCCTAG AATGGCGACA
-------------------------------------------------------------------------------
7901  TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG ATCTTCAGCA
      ACTCTAGGTC AAGCTACATT GGGTGAGCAC GTGGGTTGAC TAGAAGTCGT
-------------------------------------------------------------------------------
7951  TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG GAAGGCAAAA
      AGAAAATGAA AGTGGTCGCA AAGACCCACT CGTTTTTGTC CTTCCGTTTT
-------------------------------------------------------------------------------
8001  TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA ATACTCATAC
      ACGGCGTTTT TTCCCTTATT CCCGCTGTGC CTTTACAACT TATGAGTATG
-------------------------------------------------------------------------------
8051  TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA TTGTCTCATG
      AGAAGGAAAA AGTTATAATA ACTTCGTAAA TAGTCCCAAT AACAGAGTAC
-------------------------------------------------------------------------------
8101  AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA TAGGGGTTCC
      TCGCCTATGT ATAAACTTAC ATAAATCTTT TTATTTGTTT ATCCCCAAGG
-------------------------------------------------------------------------------
8151  GCGCACATTT C
      CGCGTGTAAA G
-------------------------------------------------------------------------------
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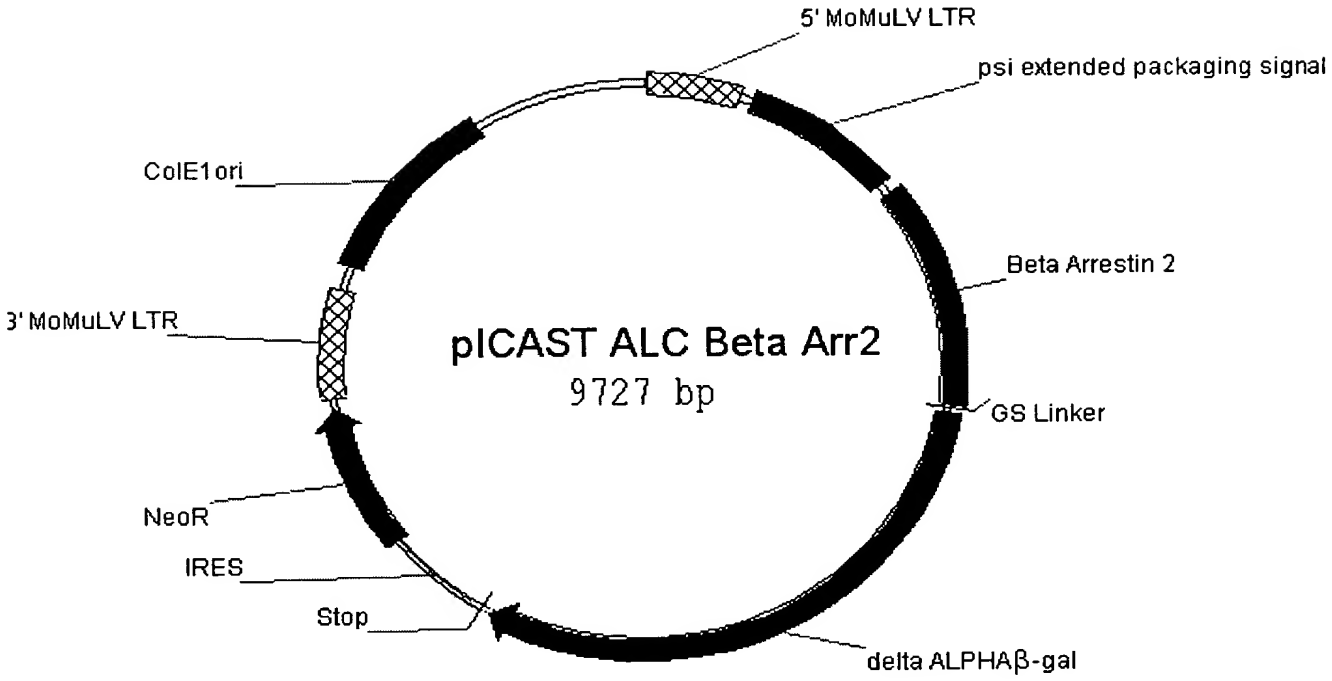

5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
Beta Arrestin 2
3' MoMuLV LTR
pICAST ALC Beta Arr2
9727 bp
GS Linker
NeoR
IRES
Stop
delta ALPHAβ-gal

Figure 14

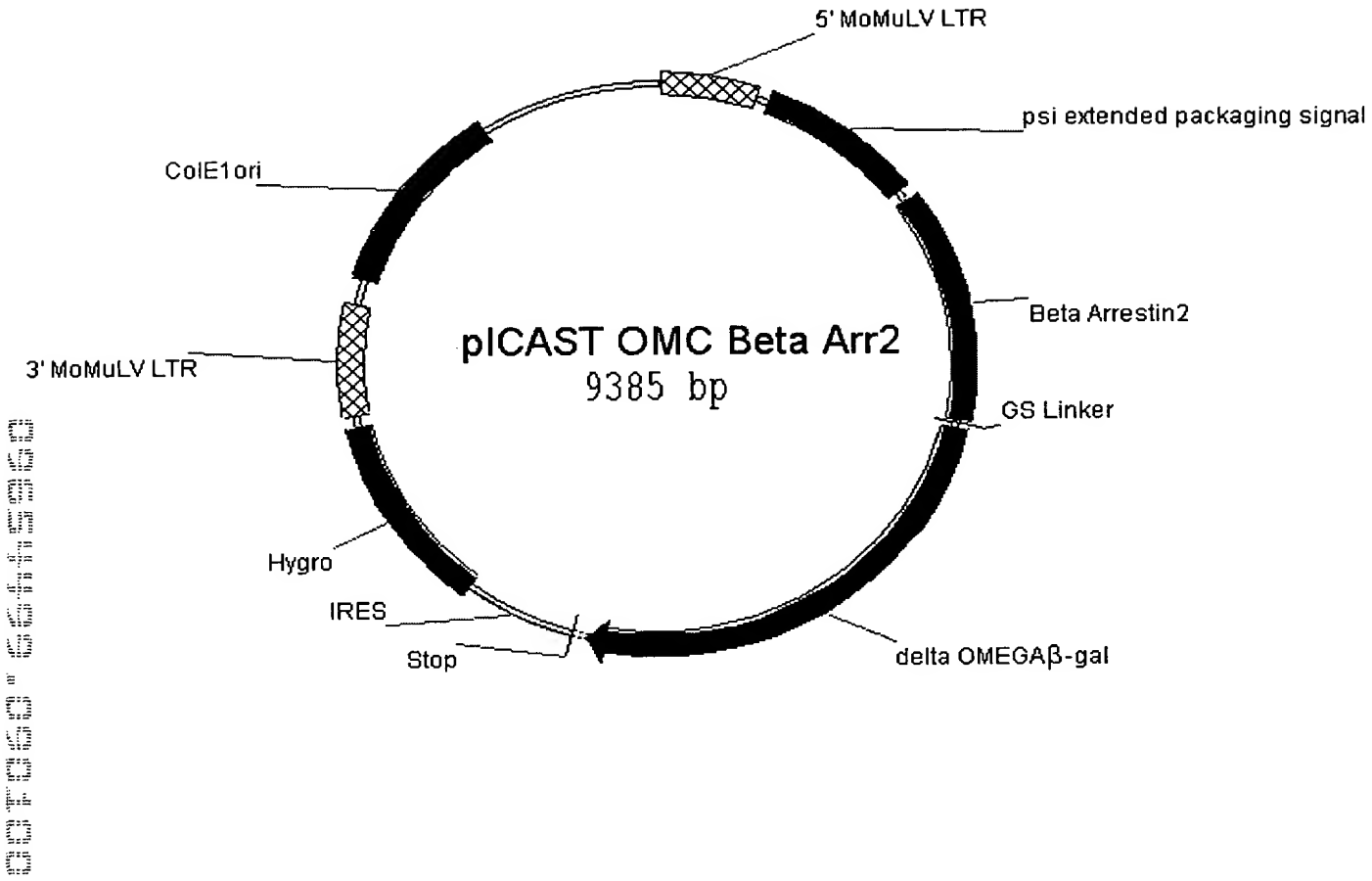

5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
Beta Arrestin2
pICAST OMC Beta Arr2
9385 bp
3' MoMuLV LTR
GS Linker
Hygro
IRES
Stop
delta OMEGAβ-gal

Figure 15

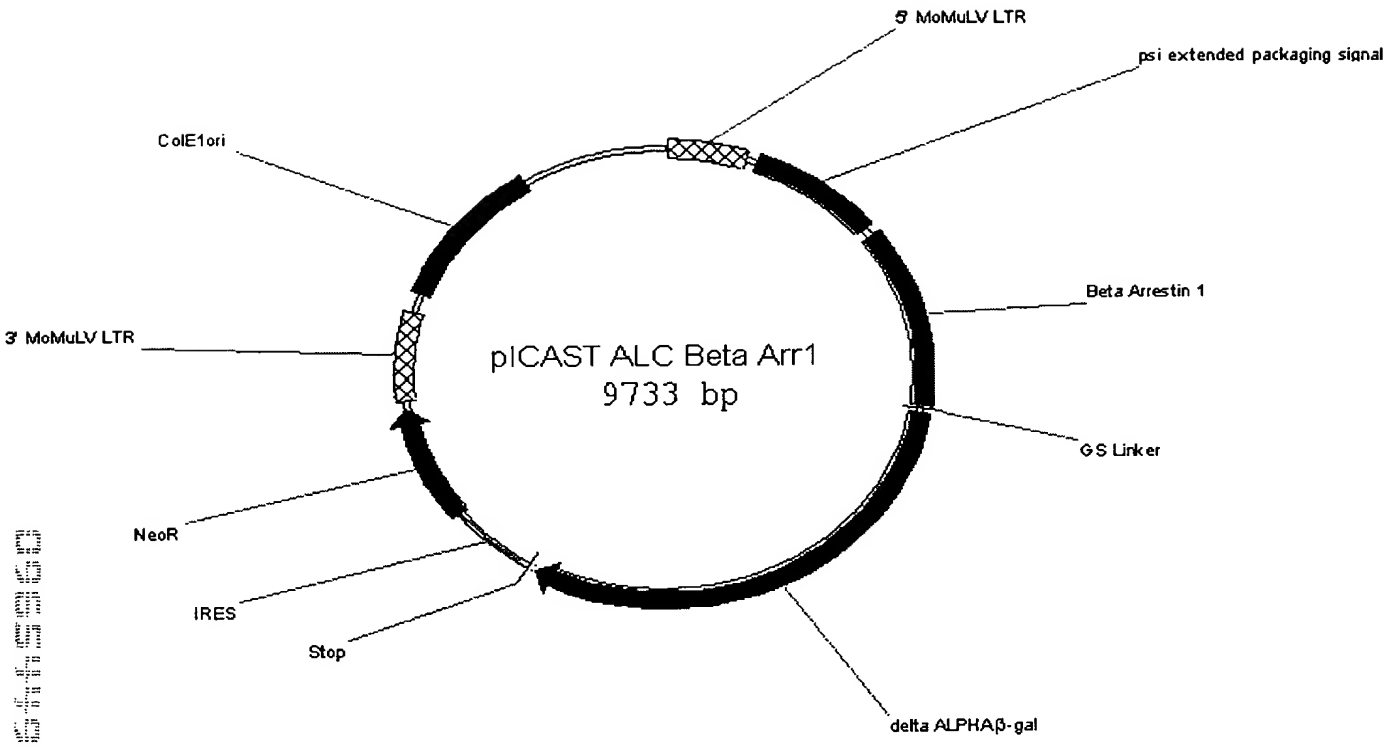

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Beta Arrestin 1
3' MoMuLV LTR
pICAST ALC Beta Arr1
9733 bp
GS Linker
NeoR
IRES
Stop
delta ALPHAβ-gal

Figure 16

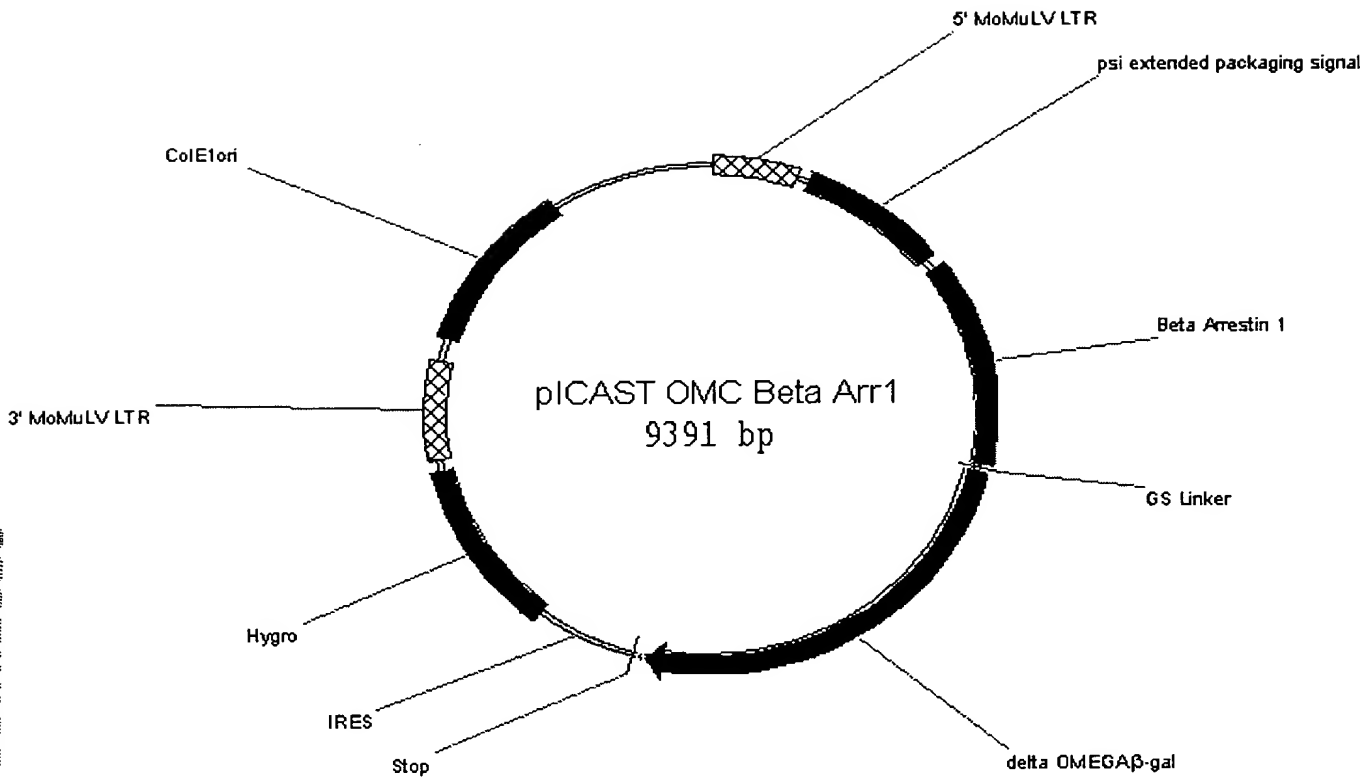

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Beta Arrestin 1
pICAST OMC Beta Arr1
9391 bp
3' MoMuLV LTR
GS Linker
Hygro
IRES
Stop
delta OMEGAβ-gal

Figure 17

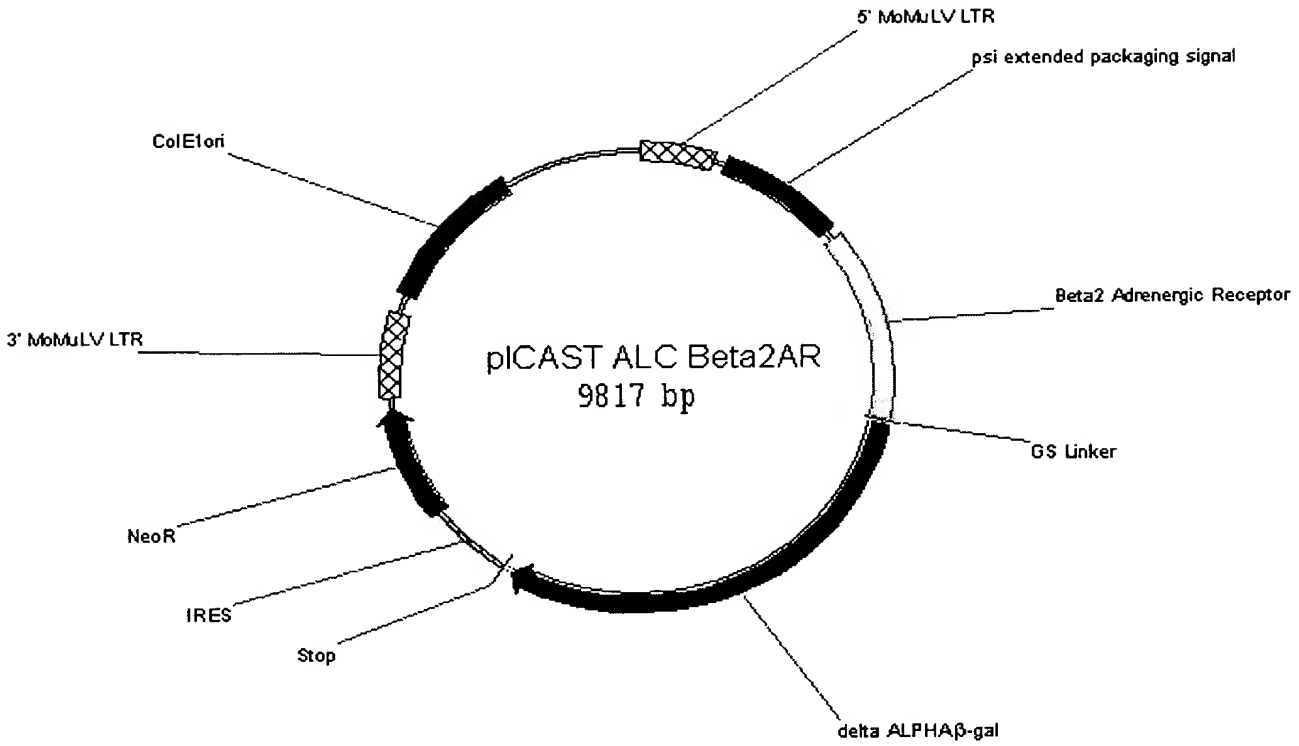

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Beta2 Adrenergic Receptor
3' MoMuLV LTR
pICAST ALC Beta2AR
9817 bp
GS Linker
NeoR
IRES
Stop
delta ALPHAβ-gal

Figure 18

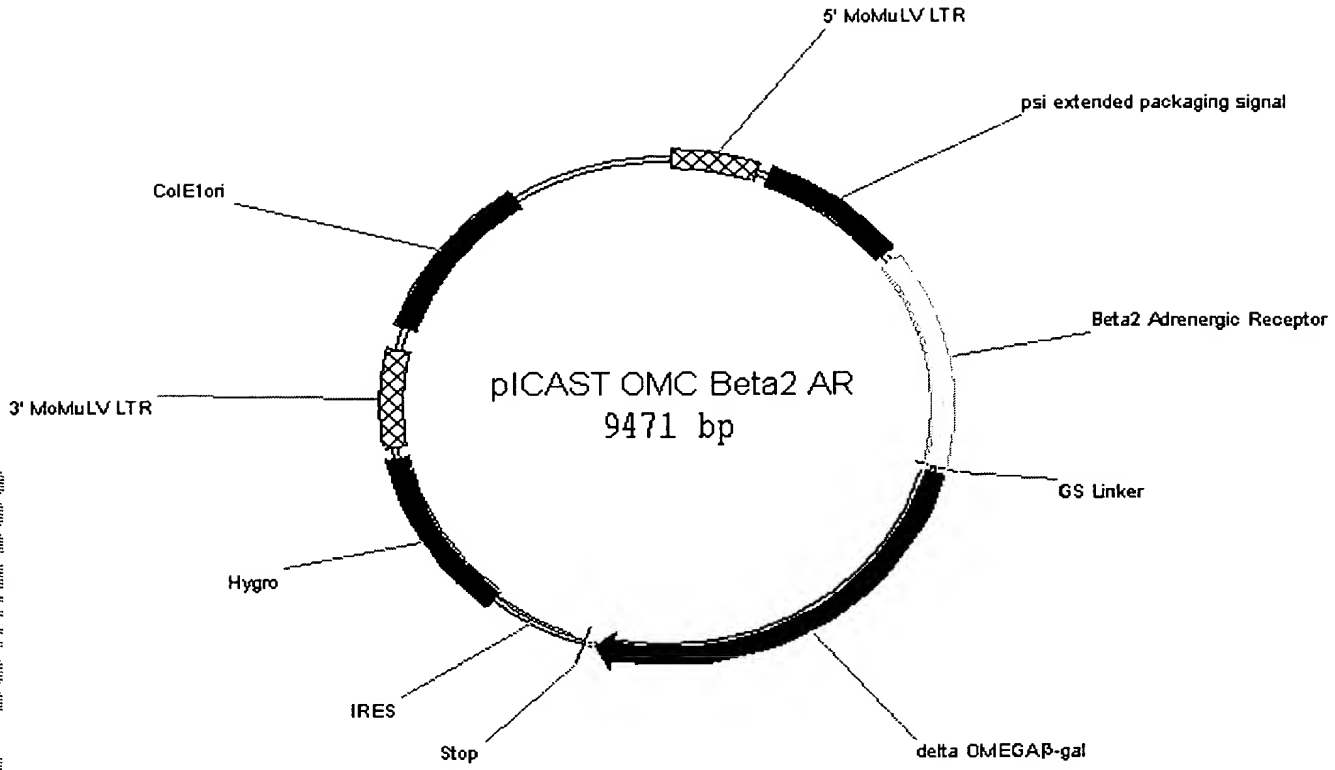

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Beta2 Adrenergic Receptor
pICAST OMC Beta2 AR
9471 bp
3' MoMuLV LTR
GS Linker
Hygro
IRES
Stop
delta OMEGAβ-gal

Figure 19

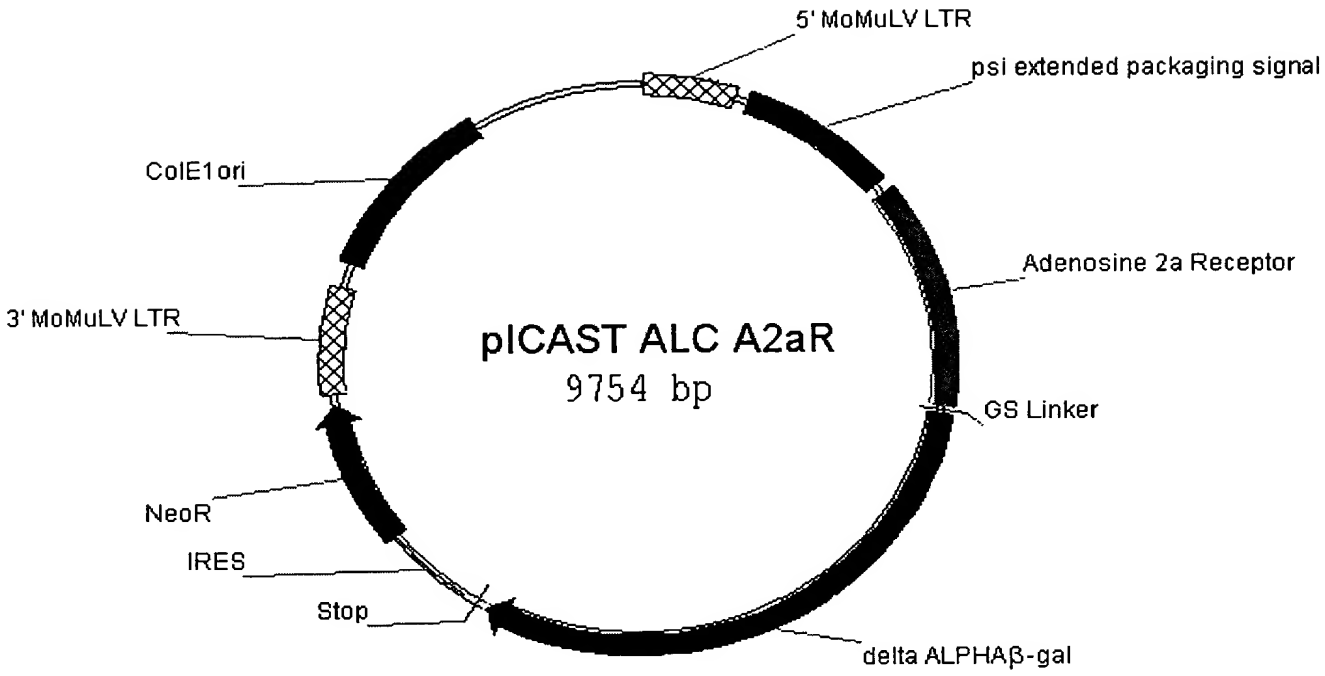

5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
Adenosine 2a Receptor
3' MoMuLV LTR
pICAST ALC A2aR
9754 bp
GS Linker
NeoR
IRES
Stop
delta ALPHAβ-gal

Figure 20

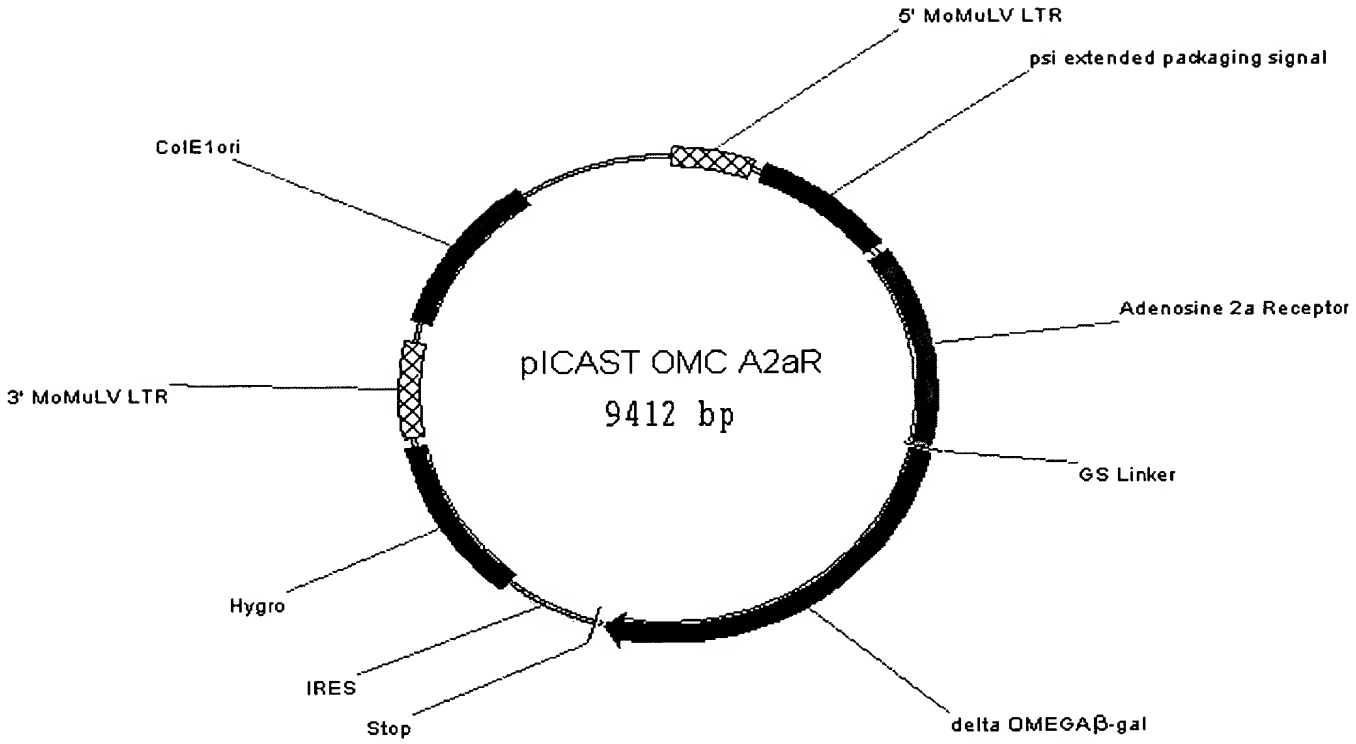

5' MoMuLV LTR
psi extended packaging signal
ColE1ori
Adenosine 2a Receptor
pICAST OMC A2aR
9412 bp
3' MoMuLV LTR
GS Linker
Hygro
IRES
Stop
delta OMEGAβ-gal

Figure 21

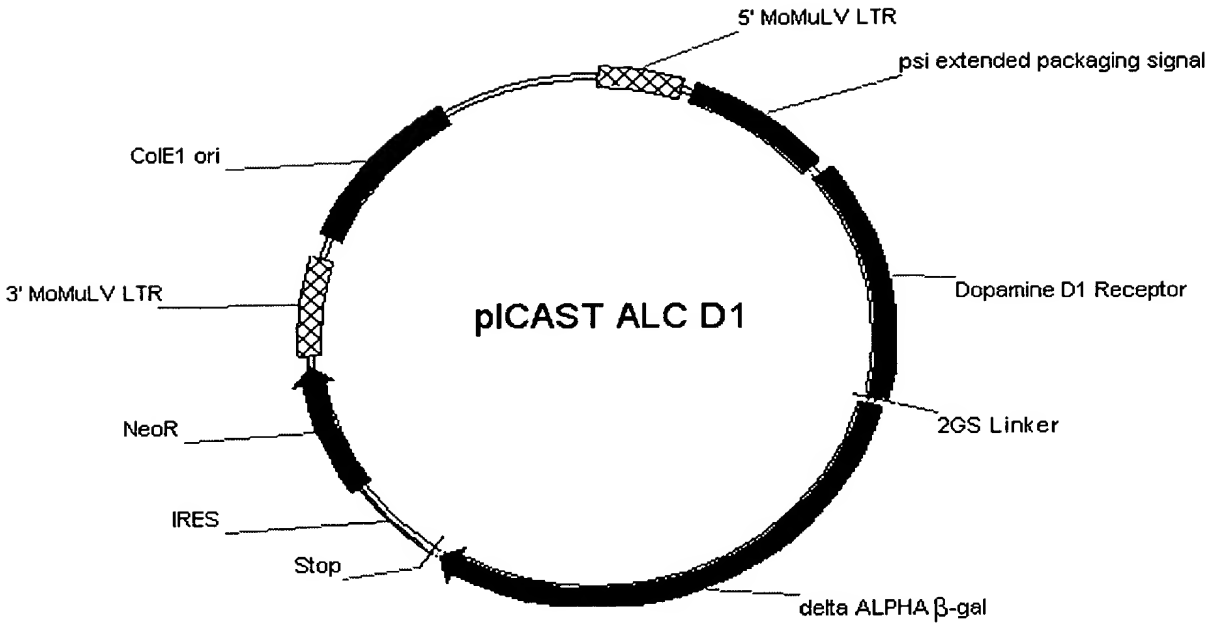
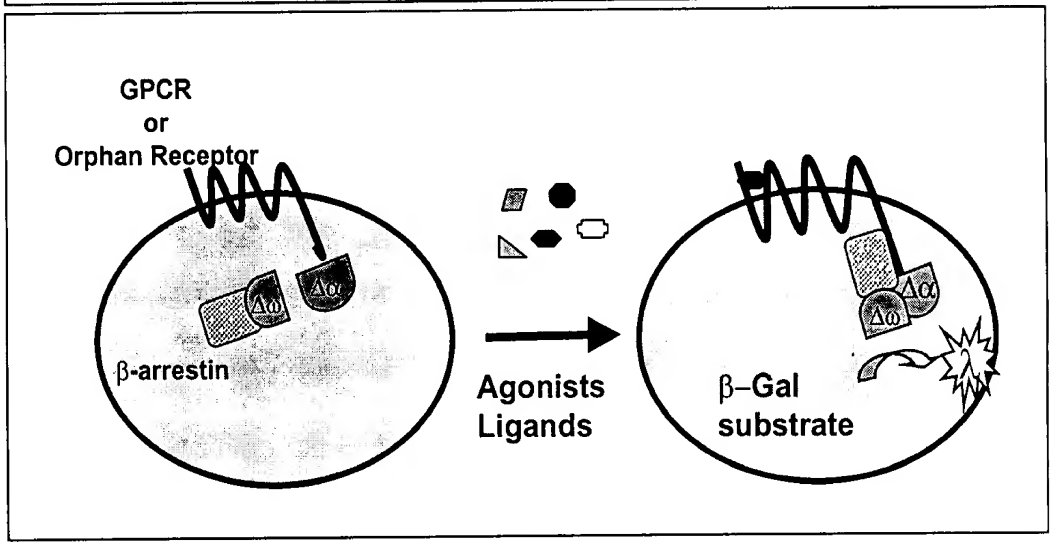

5' MoMuLV LTR
psi extended packaging signal
ColE1 ori
3' MoMuLV LTR
pICAST ALC D1
Dopamine D1 Receptor
2GS Linker
NeoR
IRES
Stop
delta ALPHA β-gal

Figure 22

Figure 23

Functional GPCR Activation Assay and Ligand Fishing for Orphan Receptors by β-galactosidase mutant complementation in ICAST™ System



Examples